

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 07:10:31 ; Search time 1927 Seconds
(without alignments)
15833.363 Million cell updates/sec

Title: US-09-918-359-6

Perfect score: 1458
Sequence: 1 atgagctcagcctcgtgga.....acctgtgctgtcaggtga 1458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_of:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sta:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	915	62.8	4695	9	HSMB02204
2	324.2	22.2	2200	9	AK023366
3	243.8	16.7	147224	2	AP003779
4	243.8	16.7	186974	2	AP003071
5	243.8	16.7	194781	2	AC019124
6	242	16.6	381	6	AX071636
7	157.8	10.8	520	11	G72237
8	137.8	9.5	194781	2	AC019124
9	79.2	5.4	162797	2	AC098981
10	75.4	5.2	162797	2	AC098981
11	68.4	4.7	70673	2	AC091258
12	67.2	4.6	2742	10	AF217002
13	62.4	4.3	4743	10	AB018253
14	60	4.1	1608	6	AX068907
15	60	4.1	7044	9	HSAB20779
16	60	4.1	7762	9	AF051946
17	60	4.1	7898	9	AF073931
18	59.8	4.1	2448	6	AX235890
19	59.8	4.1	2858	9	AK057414
20	59.8	4.1	4023	6	AX061213
21	59.8	4.1	4836	9	AB032995
22	59.8	4.1	5269	6	AX235888
23	57.6	4.0	125020	9	AF429315
24	57	3.9	2870	3	AF029249
25	55.8	3.8	125020	9	AF429315
26	53.6	3.7	6160	9	HUMCACNTA
27	52.4	3.6	885	9	HUMTRAR
28	52.4	3.6	1277	9	AF017452
29	52.4	3.6	1492	9	HSU11271
30	52.4	3.6	2932	6	E03829
31	52.4	3.6	2932	6	HUMTRAR
32	52.4	3.6	41303	9	AC005175
33	52.4	3.6	175625	2	AC068475
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36	51.8	3.6	158063	9	AP001046
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39	51.2	3.5	203691	2	AC098930
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44	50.6	3.5	5975	6	I73184
45	50.6	3.5	5975	6	I81460

ALIGNMENTS

RESULT 1
LOCUS HSM802204
DEFINITION Homo sapiens mRNA; cDNA DKFp434M0223 (from clone DKFp434M0223); partial cds.
ACCESSION AL137479
VERSION AL137479.1
KEYWORDS GI:6808092
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2000) MIPS, Am Klopfersplitz 18a, D-82152 Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFp434M0223) is available at the RZPD in Berlin.

Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY. Email: clone@r2pd.de. Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

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CDS

polyA_signal
polyA_site
BASE COUNT 1141 a 1144 c 1249 g 1161 t
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62.8% Score 915; DB 9; Length 4695;
Best Local Similarity 94.7%; Pred. No. 7.7e-182;
Matches 978; Conservative 0; Mismatches 5; Indels 50; Gaps 1;

Query Match 62.8% Score 915; DB 9; Length 4695;
Best Local Similarity 94.7%; Pred. No. 7.7e-182;
Matches 978; Conservative 0; Mismatches 5; Indels 50; Gaps 1;

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Qy 1206 GTCCAGATCTATTGTTGATTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTT 1265
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Db 1106 GCTGTGCGAGTGA 1118

RESULT 2
AK023366
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Nagatsuna, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Oho, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakawa, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Minomiy, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
Unpublished (2000)
TITLE
JOURNAL
REFERENCE
AUTHORS
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3951, Fax: 81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction: 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center

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QY 61 CCACCGGTTGGGTCGGGGGCTTCGACTCAGCCTTGGGCTGGGGAGACCAATGTTGCC 120

Db 141399 CCAGCCGGTGGGTCGGGGCCCTGGAGCTGAGCTGTGGGGTGGGAGCCAGTGCTGCC 141458

QY 121 TGGAGCTGCGGCTTCTGCTCTCAGCAGATGATGAGCAGAGGAGAGCTGACCTAC 180

Db 141459 TGGAGCTGCGGCTTCTGCTCTTACGAGATGATGAGCAGAGGAGAGGAGCTGACCTAC 141518

QY 181 TTCAGAACCTGCTGAGTCTCTGACTTCCCTCTGCTGCTGCTGACCAAGGCGCAAC 240

Db 141519 TTCAGAACCTGCTGAGTCTCTGACTTCCCTCTGCTGCTGCTGACCAAGGCGCAAC 141578

QY 241 CCGGATG 247

Db 141579 CCGGATG 141585

RESULT 5

AC019124/c

LOCUS AC019124 194781 bp DNA linear HTG 07-JUL-2000

DEFINITION Homo sapiens chromosome 11 clone RP11-554A11, WORKING DRAFT

ACCESSION AC019124

VERSION AC019124.4 GI:8568923

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 194781)

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

AUTHORS 2 (bases 1 to 194781)

REFERENCE Waterston, R.H.

TITLE Direct Submission

AUTHORS Submitted (30-DEC-1999) Genome Sequencing Center, Washington

JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Jun 16, 2000 this sequence version replaced gi:7408149.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H_NH0554A11

----- Summary Statistics -----

Sequencing vector: pLasmid: 888

Sequencing strategy: Dye-terminator Big Dye; 12% of reads

Chemistry: Dye-terminator Big Dye; 12% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 174246 bases at least Q40

Consensus quality: 180170 bases at least Q30

Consensus quality: 183510 bases at least Q20

Insert size: 197000; agarose-fp

Insert size: 192181; sum-of-contigs

Quality coverage: 3.73 in Q20 bases; agarose-fp

Quality coverage: 3.93 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. -----

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1122 1221: gap of unknown length

1222 2371: contig of 1150 bp in length

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2472 4256: contig of 1785 bp in length

4256 4257: gap of unknown length

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REFERENCE
AUTHORS

Ratus.
1 (bases 1 to 162797)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,U.R., Banks,T., Barbata,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhaq,C.,
Burck,P., Burckett,C., Burrell,K.L., Byrd,N.C., Carton,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Dean,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,D.,
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Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., Kling,L., Korah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,U., Liu,M.,
Louisege,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
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Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,L.,
Ruliz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shochterli,N.,
Stinson,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Swalek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Washington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 162797)
Worley,K.C.
Direct Submission
Submitted (08-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17062421.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GGNZ
Center clone name: CH230-112J19
----- Summary Statistics
Assembly program: Phrap, version 0.990329first call to
findhaplotype
Consensus quality: 121859 bases at least Q40
Consensus quality: 132629 bases at least Q30
Consensus quality: 141983 bases at least Q20
Estimated insert size: 130105; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 73 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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75900
75999: gap of unknown length
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77327
77426: gap of unknown length
77427
79222: contig of 1796 bp in length
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79322: gap of unknown length
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81658
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90082: contig of 1943 bp in length
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92333
92432: gap of unknown length
94341: contig of 1909 bp in length
94342
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96560
97677: contig of 1118 bp in length
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100671: gap of unknown length

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* 117722 117821: gap of unknown length
* 117822 120156: contig of 2335 bp in length
* 120157 120253: gap of unknown length
* 120254 122353: contig of 1997 bp in length
* 122354 123767: gap of unknown length
* 123768 123867: contig of 1414 bp in length
* 123868 125213: contig of 1346 bp in length
* 125214 125313: gap of unknown length
* 125314 126628: contig of 1315 bp in length
* 126629 126728: gap of unknown length
* 126729 128396: contig of 1668 bp in length
* 128397 130420: gap of unknown length
* 130421 130520: contig of 1924 bp in length
* 130521 132161: gap of unknown length
* 132162 132261: contig of 1641 bp in length
* 132262 133666: gap of unknown length
* 133667 133766: contig of 1405 bp in length
* 133767 135414: gap of unknown length
* 135415 135514: contig of 1648 bp in length
* 135515 136655: gap of unknown length
* 136656 136765: contig of 1151 bp in length
* 136766 138277: gap of unknown length
* 138278 138377: contig of 1512 bp in length

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Query Match 5.4%; Score 79.2; DB 2; Length 162797;
 Best Local Similarity 83.3%; Pred. No. 2e-06; Indels 0; Gaps 0;
 Matches 90; Conservative 0; Mismatches 18;

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QY 682 TGTACTACCTGTTGGAGTCTGCTCAAGTCTTTGGCTGGGCTGCGAGGACTACTGT 741
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62598 TGTACTACCTGTTGGAGTCTGCTCAAGTCTTTGGCTGGGCTGCGAGGACTACTGT 62539
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 CTAACCCAGCAGCGTGTGAGCGGCTCCACCCGTTGTCCTGCTGG 789
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62538 TCTACCCAGCAGCGTGTGAGCGGCTCCACCCGTTGTCCTGCTGG 62491
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RESULT 10
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 LOCUS AC098981
 DEFINITION Rattus norvegicus clone CH230-112J19, *** SEQUENCING IN PROGRESS
 AC098981.3 GI:17975740
 ACCESSION AC098981
 VERSION AC098981.3
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 162797)
 AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Albrooks, S.L., Amarantunga, H.C., Are, J.R., Banks, T., Barbara, J., Benton, J., Birmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havilap, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Huijck, S., Hune, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Koryah, J., Kovar, C., Krtovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisgied, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, S., Nguyen, N., Nickerson, E., Nnokenkwo, S., Ogulu, M., Okunolu, G., Otagunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S., Williams, G., Williamson, A., Wlarczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 162797)
 Morley, K.C.
 Direct Submission
 Submitted (08-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Dec 21, 2001 this sequence version replaced gi:17062421.

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Project Information
 Center project name: GGN2
 Center clone name: CH230-112J19

Summary Statistics
 Assembly program: Phrap; version 0.990329first call to findPhraplist
 Consensus quality: 12185 bases at least Q40
 Consensus quality: 132629 bases at least Q30
 Consensus quality: 141983 bases at least Q20
 Estimated insert size: 130105; sum-of-coverage estimation
 Quality coverage: 0x in Q20 bases; agscore-fp estimation
 Quality coverage: 1.9x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 73 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 70673)
Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,
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Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,
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Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, D.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppach, R., Seaman, S.,
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Theodore, J., Travers, M., Travis, N., Triggilio, J., Vassiliev, H.,
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Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.

Direct Submission
Submitted (11-APR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information
Center project name: L13269
Center clone name: 160_D_1

* NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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RESULT 14

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ACCESSION AJ420779
 VERSION AJ420779.1 GI:17129559
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 REFERENCE 1 (sites)
 Jaganathan, S.
 Identification and localisation of T-type voltage operated calcium subunits in human male germ cells - expression of multiple isoforms unpublished
 JOURNAL 2 (bases 1 to 7044)
 Jaganathan, S.
 Direct Submission
 Submitted (20-NOV-2001) Jaganathan S., School of Biosciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UNITED KINGDOM
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 /evidence="experimental"
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 /protein_id="CAD12646.1"
 /db_xref="GI:17129559"
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 FGOKCYGDTMNRIDPFIIVAGMMEYSLDGHVSLAIRVRLRLAIRANRPMRI
 LVTLLDTPMLGMLLFCFVFPIFGIVGVLWAGLRRCFLDSFVNNMLTEL
 PYOTGESEBEPFICSSRDNGMOKSHITGRRLMPCILGMEATVQPOAYYGDAS
 NACTNMNOYIVNCRSGDSNPNHGAINDNIGYAMIAFEVITLEGVYDQVYVMDAS
 FYNFIVTLLIVGSEFPMICLVIAVATQSETKORSSQMLREDRANHLSDSTLASE
 SEPGCEYEELIKYVGHIFRKVKRSRLVYRWQSRMKKVDPAVQDGGHQRKRG
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 EDKTSVHEEDPHRLRELOTTTELKMSCLATVPGNHLGSGSLSPILMCTAATPMPT
 KSSPFLDAPSLPDSRRSSSGDPLADOKPPASLSSSPCAPMWPBGSGAMSRRSSWS
 SLGRAPSLKRRGQGERSLISGEGSTDEADGAPRAIPRAIPRAESIDPRL
 RPAALPTKCRDGOVVALPDEFRLDSHREDAELDDSDSCCLRLKLVLEPK
 POMCSREAMALYLESPONRVSQKVIHKMFDAHVLFIFLNCVTIALERPDIP
 GSTERVELSVNITFTALFVAEMVAVVALLGLSGEHAAYLOSSNNLLDGLIVLSLD
 IYVMAASGAKIIGVLAVLRLIPLRIYISRAPIGLIVETLISLRIGNIVLI
 CCAFFITIGILVOLFKGTYTCSPDTRNISTKACRAHYRWRRRKRNPNNDGOAL
 MSFLVLSKRDGWNIMYDGLDAVGDODPVONHNPMLLFTSLIVSPFYLMAYG
 VVVENFHCRQHOEAEAREERERKRLRLERRRROAPRYADYSPRRSHSLCTS
 HYLDLFTIICVNYITSMMEHYNQPKSIDALKYCNVETIVFEALAKLVAFGR
 RPKDRMNOOLAIVLISLIGTLEETEMALPNIPTIIRIMVRLIARVILKLKMA
 TGMRLIDTVVQALPQNGILITLLELFTIYALGVELFGRLECEDPQCGSLSRHAT
 FSNFGMAFLTLRVSTGDNNGIMKDTIRECSREKHELSTYPLASPYEVTPLVAVO
 FVLVNVAVVAVLKLKLEESNKEAREDAELDALELMAQGSARVADAPRLPQESP
 GARDAAPNLVARKVSVRMLSLPNDISYMRPVVAPASAPRPLQEVEMETYGATPPLG
 VASVSPAESCAISQIPLAVSPARSGEPLHALSPRGTARSPISRLILKQEAVID
 SLKGIIDSPROTLDPAPEGKTPVAVVQGLSPSPRSPASVRETKHTFGQRCYV
 SRPAPGCEBEAADPADEEVSHITSSACPMQPTAEPHGPEASPAVAGGERDLRLYSV
 DAQGLDLPGRADQWPSAELGSGPEAKAWGPDEAPALCARKKKMSPPCISVEP

BASE COUNT 1209 a 2393 c 2216 g 1226 t
 ORIGIN

Query Match 4.1%, Score 60; DB 9; Length 7044;
 Best Local Similarity 47.6%; Pred. No. 0.02;
 Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

PAEDGSAARPSAAEGSTLLRRRTPSCAETPHRDSLPEITGSGAGDPPAKGRMGA
 SCRAEHLTVSFAFEPDLIDVPGSDPDLDSHVSHTPESSRASSGAILVLEPPSEPPM
 PYGDPPEKRRGLYTPQCPLEKRGSSATPABGGADBPV"

QY 531 CTTTCGGCCACTACTACTTGTACATCCGCGGGAACCTCATCGCCCTGGCAACCTGGTG 590
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 286 CTTGCTGACACCACTGCTGACGACGACGACGACGACGACGACGACGACGACGACG 345
 QY 591 TCCATTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 346 ACCCTGGGATGCTGCGGCTGTGAGACGCTGAGTCGCGCTCGACCG--CTGCAAC 402
 QY 651 ATCTGGGATGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 403 ATCTGGGAGGCTTGGACGCTTGAATTTGCGCTTTTGGGAGATGCTATCAAG 462
 QY 711 GTCCTTGGCCCTGCGGCTGCGGAGGTACCTGCTACCCAGCAACGCTGTTGACGGCTC 770
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 463 ATGCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
 QY 771 CTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 523 GATTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 581
 QY 831 CCGCATGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 582 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635
 QY 891 GATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 950
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 636 CGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695
 QY 951 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 696 CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755
 QY 1011 CATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 DB 756 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
 QY 1071 GAGCTTGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
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 DB 816 GACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857

Search completed: October 8, 2002, 08:56:08
 Job time : 2824 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 8, 2002, 07:11:41 : Search time 1612 Seconds
(without alignments)
12207.344 Million cell updates/sec

Title: US-09-918-359-6

Perfect score: 1458
Sequence: 1 atgagctcagcctctgtgga.....acctgtgctgtcaggtga 1458

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_estlun:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estro:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_liv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	532.8	36.5	581	9	BE141734 OVO-HT010
C 2	492.6	33.8	499	9	AM177543 RC4-CT015
C 3	415.4	28.5	431	9	AA309878 EST180740
C 4	390	26.7	994	10	BF537032 602048936
C 5	365.2	25.0	410	9	BE168889 QV1-HT051
C 6	358.8	24.6	578	9	AM178598 RC0-HT011
C 7	340	23.3	465	10	BI340329 365560 MA
C 8	329	22.6	1080	10	BG681393 602627753
C 9	309.2	21.2	632	10	BM049977 603624491
C 10	275.8	18.9	350	9	AM814045 RC6-ST019
C 11	270.8	18.6	282	9	AM845954 RC4-CT015
C 12	268.2	18.4	922	10	AM845954 RC4-CT015
C 13	267.2	18.3	396	9	AL528343 AL528343
C 14	267.2	18.3	416	9	AV668288 AV668288
C 15	250.4	17.2	489	10	BG385307 306972 MA
C 16	243.2	16.7	1184	10	BI490867 603031843
C 17	241	16.5	894	10	BI456213 603172992

C 18	207.8	14.3	262	9	AM177528 RC4-CT015
C 19	207.6	14.2	673	9	BM216125 BM216125
C 20	178.8	12.3	596	10	BM231050 K0304E05
C 21	174	11.9	338	10	BF850563 PM1-EN006
C 22	169.4	11.6	434	9	AM178475 AM178475
C 23	163.6	11.2	852	10	BI107285 BI107285
C 24	151.6	10.4	178	10	BF330244 BF330244
C 25	141.4	9.7	579	9	AM174364 AM174364
C 26	134.6	9.2	691	9	AL632626 AL632626
C 27	101.2	6.9	631	9	AV883460 AV883460
C 28	94.4	6.5	580	9	AL528344 AL528344
C 29	82	5.6	383	10	BF552166 BF552166
C 30	74.8	5.1	507	10	BI855258 BI855258
C 31	68.4	4.7	461	12	AZ854774 AZ854774
C 32	68	4.7	394	10	BI045473 BI045473
C 33	67.2	4.6	341	9	AM3221173 AM3221173
C 34	63.6	4.4	545	10	BE074505 BE074505
C 35	63.2	4.3	159	9	AM867176 AM867176
C 36	60.8	4.2	833	10	BI160381 BI160381
C 37	59.8	4.1	663	9	AL133778 AL133778
C 38	59.8	4.1	644	10	BG399273 BG399273
C 39	59	4.0	622	10	BF513282 BF513282
C 40	58.4	4.0	643	9	BB613655 BB613655
C 41	57.8	4.0	579	10	BI682620 BI682620
C 42	56.8	3.9	441	10	BF740717 BF740717
C 43	56	3.8	1049	9	AL550149 AL550149
C 44	55.6	3.8	619	12	FR0006820 FR0006820
C 45	55.4	3.8	354	12	FR0013559 FR0013559

ALIGNMENTS

RESULT 1
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LOCUS BE141734 581 bp mRNA linear EST 21-JUN-2000
DEFINITION OVO-HT0101-061099-032-h12 HT0101 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE141734
VERSION BE141734.1 GI:8604455
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 581)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QVO-HT0101-061099-032-h12&t3=1999-10-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 580.
Location/Qualifiers
1..581
/organism="Homo sapiens"

FEATURES
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Db 358 CGGGGCTCTCTCAGATGACGGTGGACCTCTTGTTCAGGATGTCCTCGAGAGGCCA 417
 QY 1400 GGGAGATGATCTACAGAGAGGCTGAGCCAGACCCGACCTGTGGC 1447
 Db 418 CGGAGAGAGGCTGATGAGAGAGTGGACCCAGCCGACCTGTGAGC 465

RESULT 8
 BG681393 1080 bp mRNA linear EST 01-MAY-2001
 LOCUS 602627753F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752492 5',
 DEFINITION mRNA sequence.
 ACCESSION BG681393
 VERSION BG681393.1 GI:13912790
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1080)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLNL0610 row: 3 column: 13
 High quality sequence stop: 829.

FEATURES
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 Location/Qualifiers
 1..1080
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4752492"
 /clone_lib="NCI_CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 218 a 235 c 318 g 249 t
 ORIGIN
 Query Match 22.6%; Score 329; DB 10; Length 1080;
 Best Local Similarity 92.0%; Pred. No. 5.8e-62;
 Matches 369; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

QY 143 AGCAGATGATGGCAGAGAGGAGGCTGACCTACTTCGAGAACTTCCTGATCTC 202
 Db 158 AGCAGATGATGGCAGAGAGGAGGCTGACCTACTTCGAGAACTTCCTGATCTC 217
 QY 203 TGACTTCCTCCCTGCTGCTGCTGACGACGCAACACCCCGATGATATTCCTGCGT 262
 Db 218 TGACTTCCTCCCTGCTGCTGCTGACGACGCAACACCCCGATGATATTCCTGCGT 276
 QY 263 ATTCCAGAAACCGGCTATGCCATCTTCTTCACTGATGATGAGAACTGT 322
 Db 277 ATTCCAGAAACCGGCTATGCCATCTTCTTCACTGATGATGAGAACTGT 336
 QY 323 TTCTGATGAACTCTGACAGACCATCTTCACTGATGATGAGAACTGT 382
 Db 337 TTCTGATGAACTCTGACAGACCATCTTCACTGATGATGAGAACTGT 396
 QY 383 CTCGCCAGACCTGCTGTTTGGAGGGGGGAGACCCGGGGCTGCTTGAAGTCTAT 442
 Db 397 CTCGCCAGACCTGCTGTTTGGAGGGGGGAGACCCGGGGCTGCTTGAAGTCTAT 456

QY 443 CCTCCATGTGGGAGAGAGGAGGCTTCCCTCAGGC-CACCCGCGAGGCCGAGTACC 501
 Db 457 CCTCCATGTGGGAGAGAGGAGGAGGCTTCCCTCAGGCAGATGTGGGTGAACCCCAAGACT 516
 QY 502 AGTCTCCGTTTCTGACAGAGCCGCAAGTTCTTCTGCGCCAC 542
 Db 517 TGCTGACAGTGTCTCAGAGAGTCCAGCTGACAGCTCCAC 557

RESULT 9
 BM049977 632 bp mRNA linear EST 07-NOV-2001
 LOCUS 603624491F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5450134 5',
 DEFINITION mRNA sequence.
 ACCESSION BM049977
 VERSION BM049977.1 GI:16779244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 632)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCMD/DTP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLNL938 row: f column: 23
 High quality sequence stop: 627.

FEATURES
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 Location/Qualifiers
 1..632
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5450134"
 /clone_lib="NIH_MGC_40"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;
 Site: 2: EcoRI; cDNA made by oligo-dT priming.
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 104 a 175 c 189 g 164 t
 ORIGIN
 Query Match 21.2%; Score 309.2; DB 10; Length 632;
 Best Local Similarity 99.0%; Pred. No. 1e-57;
 Matches 311; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 476 AGGCCACCGCGGAGGCGCGATACAGTCTCCGTTTGCAGAGCCGCGGATCTCTT 535
 Db 83 AGAGACCGCGGAGGCGCGATACAGTCTCCGTTTGCAGAGCGCGGATCTCTT 142
 QY 536 CGGCCACTACTTCTTGAATCTGGGAACTCATGCGCCCTGGCAACCTGGTGTCCAT 595
 Db 143 CGGCCACTACTTCTTGAATCTGGGAACTCATGCGCCCTGGCAACCTGGTGTCCAT 202
 QY 596 TTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
 Db 203 TTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 262
 QY 656 GGGATTCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715

Label	Sequence	Position
Db	GGGGATTCTCAACATGCGCTCATTTGTACTACTCTTGGAGATGCTGCTCAAGGCTT	322
Db	GGGGATTCTCAACATGCGCTCATTTGTACTACTCTTGGAGATGCTGCTCAAGGCTT	322
Qy	TGCCCTGGGCGCTGGAGGGTACCTGTCTTACCCAGCAACGTGTTTGACGGGCTCTCAC	775
Db	TGCCCTGGGCGCTGGAGGGTACCTGTCTTACCCAGCAACGTGTTTGACGGGCTCTCAC	382
Qy	CGTTGCTCTGCTGG	789
Db	CGTTGCTCTGCTGG	396

RESULT	10
Locus	AM814045
Definition	R6-570398-081199-021-A12 ST0198 Homo sapiens CDNA, EST 17-MAY-2000
Accession	AB814045
Version	AM814045.1 GI:7907039
Keywords	EST.
Source	human.
Organism	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (Phases 1 to 350)	Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.H. Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsushima, A., Bata, G.S., Simpson, D.I., Brumstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Contact: Simpson A.J.G.	
20202663		

TITLE	JOURNAL	MEDLINE	COMMENT
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496 (2000)	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-RC6-ST0198-081) 199-021-A126t3-1999-11-08&tt=1) Seq primer: puc 18 forward High quality sequence stat: 11 High quality sequence stop: 349. Location/Qualifiers 1..350

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0198"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTEP5 PCR (U.S. Letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
62 a 102 c 92 g 94 t

```

Query Match	18.9%	Score 275.8	DB 9	Length 350
Best Local Similarity	99.3%	Pred. No 1.8e-50		
Matches 277	Conservative 0	Mismatches 2	Indels 0	Gaps 0
476	AGGCAACCGCGGAGCGCCGATACAGATCCGCTTTCGACAGAGCCCAAGTCCCTCTT	535		
72	AAGGACACCGCGGAGCGCCGATACAGATCCGCTTTCGACAGAGCCCAAGTCCCTCTT	131		

QY	536	CGGCACACACACTTTGACCTACCTGGGGAACCTATGCGCTGGCAAAACCGGTGCAT	598
Db	132	CGGCACACACACTTTGACCTACCTGGGGAACCTATGCGCTGGCAAAACCGGTGCAT	194
QY	536	TTGCGTGTTCCTGATGCTGGATGACAGATGCTGCTGCTGAGCGATGACCTTCAATCCT	658
Db	192	TTGCGTGTTCCTGATGCTGGATGACAGATGCTGCTGCTGAGCGATGACCTTCAATCCT	254
QY	656	GGGGAATTCACACGCGCTTCATTTGTGTACTTACTGTTGAGTGTGCTGCTCAAGTCTT	718
Db	252	GGGGAATTCACACGCGCTTCATTTGTGTACTTACTGTTGAGTGTGCTGCTCAAGTCTT	314
QY	716	TGACCTGGGCGCTGCAGAGGTACTGTCTTACCCAGCAAA	754
Db	312	TGACCTGGGCGCTGCAGAGGTACTGTCTTACCCAGCAAA	350

RESULT	1.
AM845954/c	
LOCUS	282 bp mRNA linear EST 19-MAY-2006
DEFINITION	Rc4-Ct0159-130999-001-F01 CT0159 Homo sapiens CDNA, mRNA sequence.
ACCESSION	AM845954
VERSION	AM845954.1 GI:7941471
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 282)	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M. R., Nagai, M. A., da Silva, W. Jr., Zaigo, M. A., Bordini, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsumura, A., Bata, G. S., Simpson, D. H., Brunsfeld, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
COMMENT	20202663	
	Contact: Simpson A.J.G.	

COMMENT	
Contact:	Simpson A.J.G.
	Laboratory of Cancer Genetics
	Ludwig Institute for Cancer Research
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel:	+55-11-2704922
Fax:	+55-11-2707001
Email:	asimpson@ludwig.org.br
	This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL.
	(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6tz=RC4-CI0159-130)
	999-001.F016t3-1999-05-13&ta=1)
Seq primer:	puc 18 forward
	high quality sequence stop: 247.
FEATURES	
source	1..282
	Location/Qualifiers

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BASE COUNT      72 a      85 c      75 g      50 t
ORIGIN
Query Match      18.6%      Score 270.8;      DB 9;      Length 282;
Best Local Similarity 99.3%      Pred. No. 2e+49;
Matches 272;      Conservative 0;      Mismatches 2;      Indels 0;      Gaps 0;

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DE Human EST-derived coding sequence SEQ ID NO: 963.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
OS Homo sapiens.
XX
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2001; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI: 2001-476164/51.
XX P-PSDB; AAM24447.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 1: Page 756-757; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
XX Sequence 1734 BP; 315 A; 451 C; 531 G; 436 T; 1 other:
SQ
Query Match 51.6%; Score 752.4; DB 22; Length 1734;
Best Local Similarity 99.7%; Pred. No. 1.2e-176;
Matches 753; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 8 GCTCAGGCTTTGCTGCTGCGGCTGCGAGGCTGCTGCTTACCCAGCAGCTTTGA 67
QY 764 CGGGCTCTCAGCCTGCTGCTGCGAGGCTGCGAGGCTGCTGCTGCTGCTGCG 823
DB 68 CGGGCTCTCAGCCTGCTGCTGCGAGGCTGCGAGGCTGCTGCTGCTGCTGCG 127
QY 824 ACATGACCCGCGATGCTGAACATGCTACGTCGCTTCCGCTATCATCCAGCA 883
DB 128 ACATGACCCGCGATGCTGAACATGCTACGTCGCTTCCGCTATCATCCAGCA 187
QY 884 TGAAGCCGATGCGGCTGCTGCGAGGCTGCGAGGCTGCTGCTGCTGCTGCG 943
DB 188 TGAAGCCGATGCGGCTGCTGCGAGGCTGCGAGGCTGCTGCTGCTGCTGCG 247
QY 944 TTGGCGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
DB 248 TTGGCGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
QY 1004 GAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
DB 308 GAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
QY 1064 CCGTGTGGAGCTTGGAGCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1123

DB 368 CCGTGTGGAGCTTGGAGCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 427
QY 1124 CCGTGTGGAGCTTGGAGCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1183
DB 428 CCGTGTGGAGCTTGGAGCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 487
QY 1184 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
DB 488 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
QY 1244 CTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
DB 548 CTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
QY 1304 ACCCGCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1363
DB 608 ACCCGCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 1364 TGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
DB 668 TGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 1424 TGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1458
DB 728 TGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
RESULT 5
AAV59610
ID AAV59610 standard; DNA; 1751 BP.
XX
XX AAV59610;
XX
XX 06-JAN-1999 (first entry)
XX
XX Human secreted protein gene 100 clone H10AB52.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
XX WO9839448-A2.
XX
XX 11-SEP-1998.
XX
XX 06-MAR-1998; 98WO-US04493.
XX
XX 02-OCT-1997; 97US-0061060.
XX PR 07-MAR-1997; 97US-0038621.
XX PR 07-MAR-1997; 97US-0040161.
XX PR 07-MAR-1997; 97US-0040162.
XX PR 07-MAR-1997; 97US-0040163.
XX PR 07-MAR-1997; 97US-0040333.
XX PR 07-MAR-1997; 97US-0040334.
XX PR 07-MAR-1997; 97US-0040335.
XX PR 07-MAR-1997; 97US-0040336.
XX PR 07-MAR-1997; 97US-0040626.
XX PR 11-APR-1997; 97US-0043311.
XX PR 11-APR-1997; 97US-0043312.
XX PR 11-APR-1997; 97US-0043313.
XX PR 11-APR-1997; 97US-0043314.
XX PR 11-APR-1997; 97US-0043568.
XX PR 11-APR-1997; 97US-0043569.
XX PR 11-APR-1997; 97US-0043576.
XX PR 11-APR-1997; 97US-0043578.
XX PR 11-APR-1997; 97US-0043580.

Db 361 TCGTCGTGCAATCTGGGTCACACTGTTTCTGAGCCCTGATCTGTGAGAACTTCTTCAACAG 420
 Qy 1300 TGGAGACCCCGCAGACCACTGACAGCCCTTGTGTGGAGACCCCAAGAGCCACTTACAGATG 1359
 Db 421 TGGAGACCCCGCAGACCACTGACAGCCCTTGTGTGGAGACCCCAAGAGCCACTTACAGATG 480
 Qy 1360 ACTGTGAGAGCTCTGTCAGAGATATCTGAGAGAGCCGAGAGATGAGTACACAGAG 1419
 Db 481 ACTGTGAGAGCTCTGTCAGAGATATCTGAGAGAGCCGAGAGATGAGTACACAGAG 540
 Qy 1420 AGGCTGAGAGCCAGACCCGACACTGTGCTGTGACAGTGA 1458
 Db 541 AGGCTGAGAGCCAGACCCGACACTGTGCTGTGACAGTGA 579

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 ID AAI59959 standard; cDNA; 966 BP.
 AC AAI59959;
 XX
 DT 22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 3948.

Human; nootropic; immunosuppressant; cytosolic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; KW chemokine; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US34263.

21-JAN-2000; 2000US-0488725.
 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0683036.
 PR 29-NOV-2000; 2000US-0727344.

(HYSEQ) HYSEQ INC.

Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 Zhao QH, Zhou P, Goodrich R, Drmanac RT;

WPI: 2001-442253/47.

P-PSDB: AAM4803.

Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -

Claim 1; SEQ ID NO 3948; 10078bp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytosolic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localized neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

Sequence 966 BP; 170 A; 276 C; 270 G; 250 T; 0 other;

Query Match 33.2%; Score 484; DB 22; Length 966;

Best Local Similarity 76.1%; Pred. No. 3.3e-110; Matches 729; Conservative 0; Mismatches 10; Indels 219; Gaps 2;

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 Db 9 AATTCGCTGAGTCTGTGACTTCCCTCTGAGTGTGCTGACACGCGCAACACCCGAT 68
 Qy 247 GTGATGATTCCTGCGGATTCACAAAGACCGGCGCTATGCCATCTTCTATGTTCACT 306
 Db 69 GTTTGATTCCTGCGGATTCACAAAGACCGGCGCTATGCCATCTTCTATGTTCACT 128
 Qy 307 GTGATGAGAGCTGTTCTGATGAACTGCTGACAGCATCATCTACAGTTCGCGG 366
 Db 129 GTGATGAGAGCTGTTCTGATGAACTGCTGACAGCATCATCTACAGTTCGCGG 188
 Qy 367 GGCTACCTGATGAAATCTCTCCAGACCTCGCTGTTGGAGCGGCTGGAAACCGGGCT 426
 Db 189 GGCTACCTGATGAAATCTCTCCAGACCTCGCTGTTGGAGCGGCTGGAAACCGGGCT 248
 Qy 427 GCCTTGAAGTCTATCCCTCCAGACCTGTTGGAGCGGCTGGAAACCGGGCT 479
 Db 249 GCCTTGAAGTCTATCCCTCCAGACCTGTTGGAGCGGCTGGAAACCGGGCT 308
 Qy 480 ----- 479
 Db 309 GTGAGGCCCGAGAACTTGTCTGACAGTGTCTTCAAGAGTCCAGGTGACAGTCCACAAA 368
 Qy 480 ----- 479
 Db 369 CAGGCCATGATGAGAGAGGTGCTTCTATGCAAGTCTTCTGCTCACTGAGAGATT 428
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 Db 489 TACCAGTCTCTTCTTCTGACAGAGCGCCCAATCTCTTGGCCACTACTACTTGAATAC 548
 Qy 558 CTGGGGAACCTCATCGCCCTGCGCAAACTGTGTCTTCTTCTGCTGTGCTGGAT 617
 Db 549 CTGGGGAACCTCATCGCCCTGCGCAAACTGTGTCTTCTTCTGCTGTGCTGGAT 608
 Qy 618 GCAGATGTGCTGCTGCTGCTGACGCTGATGATCTTCACTTCTGAGTCTGCTTTC 677
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 Qy 678 ATTGTACTACTGTTGAGATTCTGCTCAAGCTTCTTCTGCTGCTGCTGCTGCTG 737
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 Qy 738 CTGTCCTACCCAGCAACGTTTGAAGGCGCTGCAACCGTGTCTCT 784
 Db 729 CTGTCCTACCCAGCAACGTTTGAAGGCGCTGCAACCGTGTCTCTGCTGCTTGGAG 788
 Qy 785 ----- 807
 Db 789 ATCTCAACTCTGGCTGTGTATCCGATTCACACACCGCTGAGGCGGAGATGTGGGG 848
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 Db 849 CTGCTGTGCTGTGGAGCATGACCCGATGCTGAACATGCTATGCTGTTCGCTTCTG 908

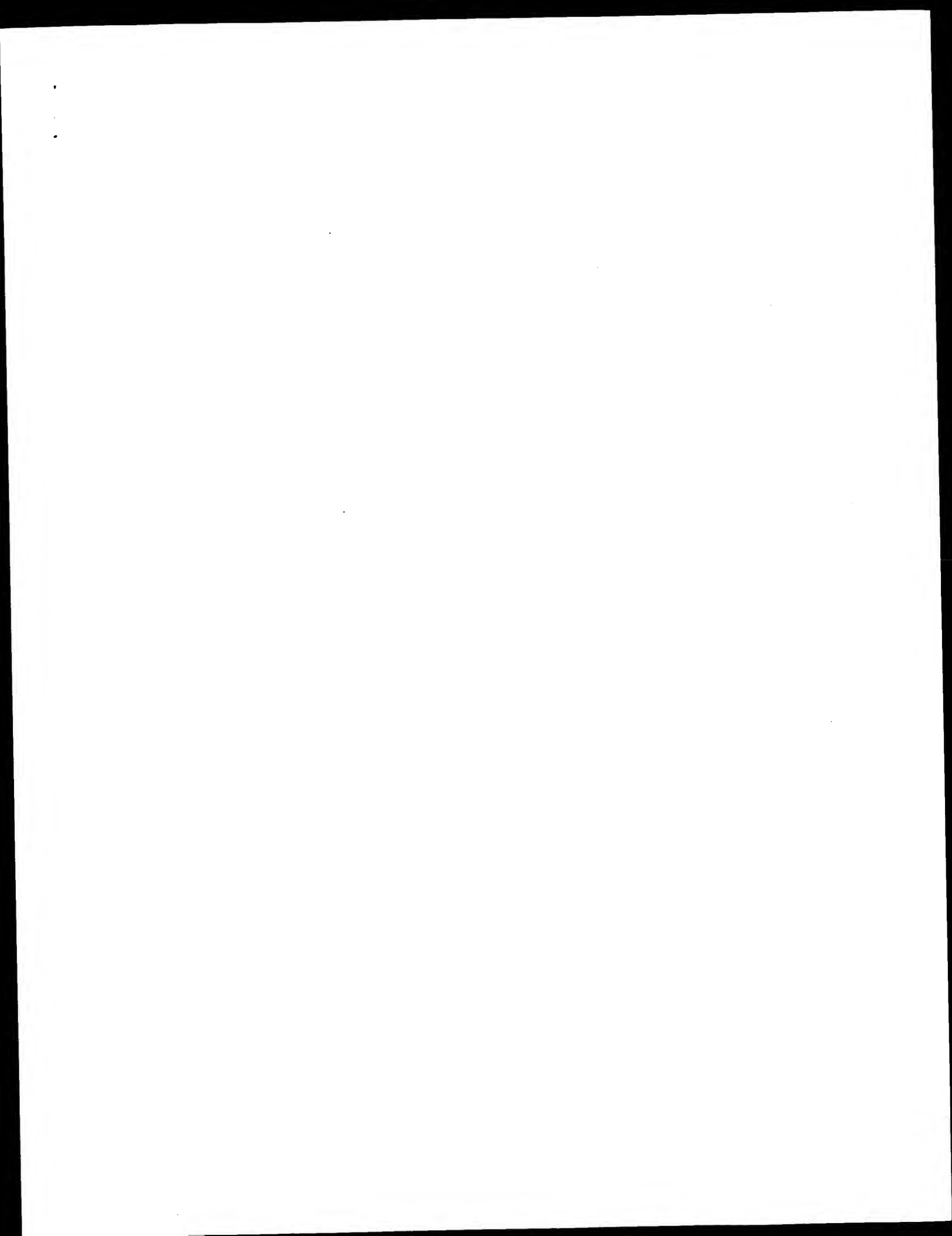
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us-09-918-359-6.rng

Page 15

[illegible]

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Job time : 222 secs



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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 08:02:31 : Search time 51 seconds
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Title: US-09-918-359-6

Perfect score: 1458

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Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/Backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	60	4.1	7898	4	US-08-984-709A-49
2	51.4	3.5	1669	4	US-08-984-709A-51
3	50.6	3.5	5975	1	US-08-404-354B-1
4	50.6	3.5	5975	1	US-08-314-083B-1
5	50.6	3.5	5975	1	US-08-435-675B-1
6	50.6	3.5	5975	1	US-08-336-257A-3
7	50.6	3.5	5975	1	US-08-884-599-1
8	49.2	3.4	6816	4	US-09-404-650-1
9	49.2	3.4	6855	4	US-09-404-650-3
10	47.4	3.3	5962	6	5386025-5
11	45.8	3.1	6048	4	US-09-634-920-3
12	45.8	3.1	6503	4	US-09-404-650-12
13	45.6	3.1	7218	1	US-08-232-463-14
14	43.8	3.0	3489	2	US-08-728-323A-1
15	43.8	3.0	6822	4	US-09-426-998-3
16	43.8	3.0	7741	4	US-09-426-998-4
17	43.8	3.0	32207	2	US-08-770-379-20
18	43.8	3.0	32207	4	US-08-757-669A-20
19	43.8	3.0	32207	4	US-09-230-371A-20
20	42.6	2.9	1138	3	US-08-581-148C-3
21	41.2	2.8	2338	2	US-08-455-543A-31
22	41.2	2.8	2338	2	US-08-223-305C-31
23	41.2	2.8	5904	1	US-07-745-206A-6
24	41.2	2.8	5904	1	US-08-455-543A-3
25	41.2	2.8	5904	2	US-08-193-078B-3
26	41.2	2.8	5904	2	US-08-223-305C-3
27	41.2	2.8	5904	2	US-08-149-097D-3

28	41.2	2.8	5904	2	US-08-311-363-6	Sequence 6, Appl
29	41.2	2.8	6575	3	US-08-949-386-3	Sequence 3, Appl
30	41.2	2.8	6575	3	US-08-450-562-3	Sequence 3, Appl
31	41.2	2.8	6575	4	US-08-984-709A-3	Sequence 3, Appl
32	40.2	2.8	1901	1	US-08-153-848-43	Sequence 43, Appl
33	40.2	2.8	1901	1	US-09-299-845A-43	Sequence 43, Appl
34	40.2	2.8	1901	4	US-09-088-337B-43	Sequence 43, Appl
35	40.2	2.8	1901	5	PCP-US93-1153-43	Sequence 43, Appl
36	40.2	2.8	2453	5	PCP-US95-07180-1	Sequence 1, Appl
37	40.2	2.8	2742	4	US-09-232-468A-1	Sequence 1, Appl
38	39.6	2.7	16442	3	US-08-781-891-208	Sequence 208, App
39	39.2	2.7	1413	4	US-08-984-709A-52	Sequence 32, Appl
40	39.2	2.7	4403765	4	US-09-103-840A-2	Sequence 2, Appl
41	39.2	2.7	4411529	4	US-09-103-840A-1	Sequence 1, Appl
42	39	2.7	836	3	US-08-674-984-1	Sequence 1, Appl
43	39	2.7	836	5	PCP-US95-15601-1	Sequence 1, Appl
44	39	2.7	7791	2	US-08-149-097D-23	Sequence 23, Appl
45	39	2.7	7808	2	US-08-149-097D-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-984-709A-49
Sequence 49, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 249...7307
OTHER INFORMATION:
US-08-984-709A-49


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STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,354B
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53192
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79..5700
OTHER INFORMATION:
US-08-404-354B-1

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Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

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QY 770 CCTACCGTGTCTCTGCTGAGGCGGAGATGTTGGGCTGCTGCTGTGGACATGA 829
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DB 1584 CGT-----GATGTGAGGCGGATCTGAGGCTGTGTGAGATCGGGGCGCATGACGC 1639
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QY 830 CCGCAGATGCTGAACATCTCATCTGTTCCGCTTCGCGATCATCCCGACGATGAGC 889
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DB 1640 CGCTGGGAGATCTCGTGTTCGGCTGCATCCGCTCGTGAAGCTTCAAGATCAACCAAGT 1699
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RESULT 4
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; Sequence 1, Application US/08314083B
; Patent No. 5686241

```

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GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,083B
FILING DATE: 28-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79..5700
OTHER INFORMATION:
US-08-314-083B-1

Query Match          3.5%; Score 50.6; DB 1; Length 5975;
Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

QY 650 CATCTGGGAGATTCTCAATCGCTCTTCACTGTTGTAAGTTCGTCCTCA 709
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DB 1464 CTTCGAAGACATCGCCATGAGTGTCTGCTCCTTACCCAGCAAGTGTGACGGGCT 769
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Db 1700 ACTGAGCTGCTGACCAACTGGTGAGCTCCCTGCTCAACTCCATCCGCTCATCGCCT 1759
QY 950 GGATCTGGGAGGCTCTACTAGCTATTGGCCATCATTTG 988
Db 1760 CGCTGCTGCTGCTGCTCTCTCTCTTCATCATCATCTTTCG 1798

RESULT 5
US-08-435-675B-1
; Sequence 1, Application US/08435675B
; Patent No. 5710250

GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,675B
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53193
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79...5700
OTHER INFORMATION:
US-08-435-675B-1

Query Match 3.5%; Score 50.6; DB 1; Length 5975;
Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

QY 650 CATCTGGGAGTCTCAACTGCGTCTTCACTGTAATCACTGTTGAGTTGGCTGCA 709
Db 1464 CTGCAAGACATCGCCAAATGAGTGGCTGCTCACTTACCATGACATGCTGCTGAA 1523
QY 710 GGTCTTTGGCCCTGGGCTGGAGGGTACCTGCTCCATCCAGCAAGCTGTTGACGGGCT 769

Db 1524 GATGTACGGGCTGGGCTCGGCCAGTACTGTGATGCTCCATCTTCAACCGCTTGCATGCTT 1583
QY 770 CCTACACGTTGCTCTGAGAGCGCGAGATGTTGGCCCTGCTGCTGGGACATGA 829
Db 1584 CGT----GGTGTGACAGCGGATCTGAGAGTGTGCTGTGGAGTGGGGCCATGACGC 1639
QY 830 CCGCATGCTGAACATGCTCATGCTGTTCGCTTCTCGGTATCATCCAGCATGAAGC 889
Db 1640 CGCTGGGCACTTCCTCGGTGGCGCTGCATCCGCTCTGAGGCTCTTCAAGATCACCAAGT 1699
QY 890 CGATGGCCGCTGGGCGCAGTACCGTCTGGGCTGGTGGAGAACATGCGCTTGGCG 949
Db 1700 ACTGAGCTGCTGCTGACCAACTGGTGAGCTCCCTGCTCAACTCCATCCGCTCATCGCCT 1759
QY 950 GGATCTGGTGGTCTACTAGCTATTGGCCATCATTTG 988
Db 1760 CGCTGCTGCTGCTGCTCTCTCTCTTCATCATCATCTTTCG 1798

RESULT 6
US-08-336-257A-3
; Sequence 3, Application US/08336257A
; Patent No. 5726035

GENERAL INFORMATION:
APPLICANT: Jay, Scott D.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,257A
FILING DATE: 07-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 54898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79...5700
OTHER INFORMATION: "product="Alpha-1 subunit of animal calcium channel"
US-08-336-257A-3

Query Match 3.5%; Score 50.6; DB 1; Length 5975;
Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

QY 650 CATCTGGGAGTCTCAACTGCGTCTTCACTGTAATCACTGTTGAGTTGGCTGCA 709
Db 1464 CTGCAAGACATCGCCAAATGAGTGGCTGCTCACTTACCATGACATGCTGCTGAA 1523
QY 710 GGTCTTTGGCCCTGGGCTGGAGGGTACCTGCTCCATCCAGCAAGCTGTTGACGGGCT 769

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 08:56:11 : Search time 59 Seconds
(without alignments)
913.064 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634
Sequence: 1 MSSACWEATGRCRLGGMMV.....PGEELTERLSOHPHILWLCR 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1671.5	63.5	22	AAM39017	Human polypeptide
2	1108	42.1	210	AAW24447	Human EST encoded
3	1020	38.7	192	AAW24828	Human secreted pro
4	922	35.0	333	AAB94563	Human protein sequ
5	784	22.8	591	AAU00502	Human TANO 437 pr
6	582.5	22.1	22	AAW40803	Human polypeptide
7	342	13.0	584	AAW67465	Amino acid sequenc
8	342	13.0	594	AAW75376	Human colon cancer
9	342	13.0	748	AAW60097	Human transport pr
10	342	13.0	816	AAW77820	Human ion channel
11	336	12.8	520	AAW23901	Rat EST encoded pr

12	208	7.9	395	22	AAM25607	Human protein sequ
13	195	7.4	2161	14	AAR33545	Sequence of the al
14	190	7.2	2161	16	AAR71001	Human neuronal cal
15	190	7.2	2161	16	AAR71002	Human neuronal cal
16	190	7.2	2161	19	AAW63137	Human calcium chan
17	190	7.2	2161	19	AAW63149	Human calcium chan
18	190	7.2	2161	21	AAW10568	Human calcium chan
19	189	7.2	724	13	AAR27648	Human CACNAIF sp1
20	189	7.2	1912	21	AAV49429	Human CACNAIF long
21	189	7.2	1912	21	AAV49430	Human neuronal cal
22	189	7.2	1912	21	AAV49430	Human neuronal cal
23	189	7.2	2270	16	AAR71010	Calcium channel al
24	189	7.2	2270	16	AAW69604	Human calcium chan
25	187.5	7.1	2044	20	AAV14595	Human T-type volta
26	187.5	7.1	2044	20	AAV14594	Human T-type volta
27	187	7.1	2251	16	AAW75009	Rabbit skeletal mus
28	186.5	7.1	2251	16	AAW75009	Human neuronal cal
29	186.5	7.1	2251	16	AAW75009	Human neuronal cal
30	186	7.1	175	22	AAW67469	Amino acid sequenc
31	186	7.1	1873	16	AAR73055	Rabbit skeletal ca
32	186	7.1	1873	18	AAW37711	Rabbit skeletal ca
33	186	7.1	1873	18	AAW18390	Rabbit skeletal ca
34	186	7.1	1873	21	AAV77544	Human neuronal cal
35	184	7.0	2138	16	AAR72607	Human calcium chan
36	184	7.0	2138	21	AAW10583	Calcium channel al
37	182	6.9	2338	21	AAW78900	Murine CACNAIF pro
38	180.5	6.9	1824	21	AAV49431	Human activated the
39	180	6.8	2034	20	AAV06300	Sequence of the al
40	178.5	6.8	1967	14	AAW33547	Human calcium chan
41	178.5	6.8	1968	19	AAW63139	Human neuronal cal
42	175.5	6.7	2237	16	AAW71006	Human calcium chan
43	175.5	6.7	2237	19	AAW63142	Human calcium chan
44	175.5	6.7	2237	21	AAW10573	Human calcium chan
45	175.5	6.7	2337	19	AAW37878	Human calcium chan

ALIGNMENTS

RESULT 1	AAW39017	standard; Protein: 552 AA.
ID	AAW39017	
XX	AAW39017;	
XX	22-OCT-2001 (first entry)	
XX	Human polypeptide SEQ ID NO 2162.	
DE	XX	
XX	Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukemia.	
OS	Homo sapiens.	
XX	XX	
PN	WO200153312-A1.	
XX	XX	
PD	26-JUL-2001.	
XX	XX	
PF	26-DEC-2000; 2000WO-US34263.	
XX	XX	
XX	21-JAN-2000; 2000US-0488725.	
PR	25-APR-2000; 2000US-0552317.	
PR	09-JUL-2000; 2000US-0598042.	
PR	19-JUL-2000; 2000US-0620312.	
PR	03-AUG-2000; 2000US-0653450.	
PR	14-SEP-2000; 2000US-0662191.	
PR	19-OCT-2000; 2000US-0693036.	
PR	29-NOV-2000; 2000US-0727344.	
XX	XX	

RESULT 3
 ID AAW74828 standard; Protein; 192 AA.
 AC AAW74828;
 XX 25-JAN-1999 (first entry)
 DE Human secreted protein encoded by gene 100 clone H10AB52.
 XX
 KM Human; secreted protein; testis; tumour; foetal brain tissue;
 KM fusion protein; cancer; central nervous system; seizure;
 KM diagnosis; neurodegenerative disease.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 192
 FT label= unknown
 XX
 PD W09839448-A2.
 XX 11-SEP-1998.
 PE 06-MAR-1998; 98WO-US04493.
 XX
 XX 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 07-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0043500.
 PR 23-MAY-1997; 97US-0043501.
 PR 23-MAY-1997; 97US-0043502.
 PR 23-MAY-1997; 97US-0043503.
 PR 23-MAY-1997; 97US-0043581.
 PR 23-MAY-1997; 97US-0043582.
 PR 23-MAY-1997; 97US-0043583.
 PR 23-MAY-1997; 97US-0043584.
 PR 23-MAY-1997; 97US-0043585.
 PR 23-MAY-1997; 97US-0043586.
 PR 23-MAY-1997; 97US-0043587.
 PR 23-MAY-1997; 97US-0043588.
 PR 23-MAY-1997; 97US-0043589.
 PR 23-MAY-1997; 97US-0043590.
 PR 23-MAY-1997; 97US-0043592.
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 PR 23-MAY-1997; 97US-0043594.
 PR 23-MAY-1997; 97US-0043595.
 PR 23-MAY-1997; 97US-0043596.
 PR 23-MAY-1997; 97US-0043597.
 PR 23-MAY-1997; 97US-0043598.
 PR 23-MAY-1997; 97US-0043599.

PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047633.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0049610.
 PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052874.
 PR 18-AUG-1997; 97US-0055724.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057659.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 DR WPI; 1998-506364/43.
 DR N-PSDB; AAV59610.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 601-602; 721pp: English.
 XX
 CC This sequence represents a secreted human protein encoded by the nucleic
 CC acid molecule designated Gene 100 from the human cDNA clone H10AB52
 CC (deposited as clone ATCC 97901 and ATCC 209047).

CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC polypeptides in a sample or by determining the amount of the new
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).

SO Sequence 192 AA:

Query Match 38.7%; Score 1020; DB 19; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.4e-91;

Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 MKPAAVAVSVTLGVQNMRAFGGLVYVYFAITGINLRGVVALPGNSSLPANGSA 354
 DB 1 MKPAAVAVSVTLGVQNMRAFGGLVYVYFAITGINLRGVVALPGNSSLPANGSA 60
 QY 355 PCGSFDELEWANNDFEALALVTLMNLAVYNNQVFLDAYRRYSGPWSKIYFVLMWLV 414
 DB 61 PCGSFDELEWANNDFEALALVTLMNLAVYNNQVFLDAYRRYSGPWSKIYFVLMWLV 120
 QY 415 SVTAVNLFALILENLFHKWDPKSHLOPLAGTPEATYQMTVELFRDILEPGEDELTER 474
 DB 121 SVTAVNLFALILENLFHKWDPKSHLOPLAGTPEATYQMTVELFRDILEPGEDELTER 180
 QY 475 LSOHPHLMICR 485
 DB 181 LSOHPHLMICR 191

RESULT 4

AA094563 ID AAB94563 standard; Protein; 333 AA.

AC AAB94563;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:15339.

KW Human; primer: detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isega T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

PI WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

XX Claim 8; SEQ ID 15339; 2537pp + CD ROM; English.

PS The present invention describes primer sets for synthesizing 5602
 XX full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dt primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination
 CC of the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

SO Sequence 333 AA:

Query Match 35.0%; Score 922; DB 22; Length 333;
 Best Local Similarity 51.0%; Pred. No. 1.1e-81;

Matches 211; Conservative 20; Mismatches 64; Indels 114; Gaps 9;

QY 82 DVMIPATSKRRAVAIFEFIVTIGSLFLMNLTAIISOPRGYLMKSLQSLPFRRLGTR 141
 DB 34 EVMIPATSKRRAVAIFEFIVTIGSLFLMNLTAIISOPRGYLMKSLQSLPFRRLGTR 93
 QY 142 AAEVLISSNVEGGAFFQATRRGPTSLRRCRAPSSSATTTLTWTGSSPQWTCFPAC 201
 DB 94 AAEVLISSNVEGGAFFQATRRGPTSLRRCRAPSSSATTTLTWTGSSPQWTCFPAC 135
 QY 202 SWCMQWCCLLSVTSSWGSSTASSLCTTCWSCCSSLPACGCTCTPATCLTGSSPLS 261
 DB 136 -----AMMEEVRSIGSV----- 147
 QY 262 CWRPEWGLSLMDMTMLNLIVFRRLIIPSKMPAAVAVSVTLGVQNMRAFGGLIYV 321
 DB 148 -----LLSAEEFQILFREL-----DRSVKREHPREPRQSPFLQSAQFL--FG----- 188
 QY 322 VYVFAIIGINLFR-----GVYALPGNSSLPANGSAPCGSFDELEWANNDFDPAAL 376
 DB 189 -HYEFDYLG-NLIALANLVSIQFVLADADVPAER-----DDF----- 225
 QY 377 VTLAMNLAVYNNQVFLDAYRRYSGPWSKIYFVLMWLVSVIYVNLFLALILENLFHKWDP 436
 DB 226 -ILMNLAVYNNQVFLDAYRRYSGPWSKIYFVLMWLVSVIYVNLFLALILENLFHKWDP 284
 QY 437 RSHLQPLAGTPEATYQMTVELFRDILEPGEDELTERLSQHPHLMICR 485
 DB 285 RSHLQPLAGTPEATYQMTVELFRDILEPGEDELTERLSQHPHLMICR 333

RESULT 5

AA000502 ID AAU00502 standard; Protein; 591 AA.

AC AAU00502;

DT 18-JUL-2001 (first entry)

DE Human TANGO 437 protein.

KW Human; TANGO 315; clone jtl9a045b02; TANGO 330; TANGO 437; TANGO 480;

KW cellular process regulator; gene therapy; mixed lymphocyte reaction;

QY 181 -TTTTTWTG-----SSPWQTCPFACSWCW----- 205
 Db 379 MMEKRSYGSVLLSAEEFOKLFNEIDRSYKHEHPREXQSPFLQSAQFLGHYYFDYIG 438
 QY 206 -----MOMCCLLSWTSS-----WGSTASSLCTTWCSCCSLPAACGCTCP 248
 Db 439 NLIALANLVISICVFLVDADVLPARDPDLGLINCFTVYLLLEMLKVFALGLRGYLS 498
 QY 249 TPATCTUG-----SSPLSCRPPEMVGLLSLMDMTMLMLIVFRFLRI 291
 Db 499 YPSVVEFGLLTVVLLVLEISTLAVYRLPHRGKRPENVGLLSLMDMTMLMLIVFRFLRI 558
 QY 292 IPSMKPMVAIVASTVGLVQNMRAAFGLIV 320
 Db 559 IPSMKPMVAIVASTVGLVQNMRAAFGLIV 587

RESULT 6
 AAM40803
 ID AAM40803 standard; Protein; 321 AA.
 AC AAM40803;
 XX
 XX 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 5734.
 XX
 XX Human; nootropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM leukemic; thrombolytic; drug screening; arthritis; inflammation;
 XX
 XX Homo sapiens.
 OS
 PN WO200153312-A1.
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 23-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Dirmann RT;
 XX
 XX WPI: 2001-442253/47.
 DR N-PSDB: AAI59959.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Example 2; SEQ ID NO 5734; 10078pp; English.
 XX
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytosolic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 SQ Sequence 321 AA;
 QY Query Match 22.1%, Score 582.5; DB 22; Length 321;
 Db Best Local Similarity 46.6%, Pred. No. 1.9e-48;
 Matches 151; Conservative 17; Mismatches 73; Indels 83; Gaps 7;
 QY 63 NPESTSLIVLLTANNPDVIRAYSKRATFFTYVIGSLFIMNLITATYQFR 122
 Db 3 NSPESTSLIVLLTANNLFLVLPAYSKRATFFTYVIGSLFIMNLITATYQFR 62
 QY 123 GYLKSLQTSLEFRRRLGTRAAFEVLSMWGEGAFPOATRGRPSTSLFCRAPSSSA-- 180
 Db 63 GYLKSLQTSLEFRRRLGTRAAFEVLSMWGEGAFPOATRGRPSTSLFCRAPSSSA-- 122
 QY 181 ---TTTTTWTG-----SSPWQTCPFACSWCW--- 205
 Db 123 QAMMEKRSYGSVLLSAEEFOKLFNEIDRSYKHEHPREXQSPFLQSAQFLGHYYFDY 182
 QY 206 -----MOMCCLLSWTSS-----WGSTASSLCTTWCSCCSLPAACGCT 246
 Db 183 LGNLIALANLVISICVFLVDADVLPARDPDLGLINCFTVYLLLEMLKVFALGLRGY 242
 QY 247 CPTATCTUG-----SSPLSC-----WRPEMVGLLSLMDMTMLMLI 284
 Db 243 LSPSNVFDGLITVYLLVLEISTLCTCHTQAGGRBWR-----LLSLMDMTMLMLI 297
 QY 285 VREFRLIIPSMKPMVAIVASTVGL 308
 Db 298 VREFRLIIPSMKPMVAIVASTVGL 321

RESULT 7
 AAB67465
 ID AAB67465 standard; Protein; 584 AA.
 AC AAB67465;
 XX
 XX 15-MAY-2001 (first entry)
 DE
 XX Amino acid sequence of a calcium channel transport polypeptide.
 DE
 XX Calcium channel transport polypeptide; calcium trafficking;
 KW neural disorder; HIV-induced dementia; immune system disorder;
 KW rheumatoid arthritis; muscular disorder; muscle contractile dysfunction;
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
 KW cardiovascular disorder; arrhythmia; renal disorder;
 KW proliferative disorder; cancer; lung carcinoma; breast cancer.
 XX
 XX Homo sapiens.
 OS
 PN WO200108635-A2.
 PD 08-FEB-2001.
 XX
 XX 27-JUL-2000; 2000WO-US20392.
 PF
 XX 28-JUL-1999; 99US-0145958.
 PR 18-AUG-1999; 99US-0149446.
 PR 14-MAR-2000; 2000US-0189064.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruden SM, Ni J, Shi Y;

XX WPI: 2001-138604/14.
 DR N-PSDB; AAF55042.
 XX
 PT New isolated nucleic acid useful for diagnosing, detecting, or treating
 PT or preventing diseases associated with anomalies in calcium trafficking
 PT across the plasma membrane -
 XX
 PS Claim 11; Page 256-257; 259pp; English.
 XX
 CC The present sequence represents a calcium channel transport polypeptide.
 CC The polynucleotides, polypeptides, and antibodies are useful for
 CC preventing, treating, or ameliorating diseases associated with anomalies
 CC in calcium trafficking across the plasma membrane. They are used to
 CC diagnose, detect and treat or prevent diseases or conditions such as
 CC neural disorders (e.g. HIV-induced dementia), immune system disorders
 CC (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile
 CC dysfunction), reproductive disorders, gastrointestinal disorders,
 CC pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal
 CC disorders, proliferative disorders, and/or cancerous diseases and
 CC conditions (e.g. lung carcinoma or breast cancer).
 XX
 SQ Sequence 584 AA;
 Query Match 13.0%; Score 342; DB 22; Length 584;
 Best Local Similarity 25.4%; Pred. No. 1.5e-24;
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;
 QY 60 YFQNPESLTSILVLTANNPDVMIAPSKRAVAIFETVFGSLMLNLTAAIIS 119
 DB 30 YFSTLSTNSIVSLFVLITLTFNPDVMPYSRNWSCVFETVYLSIELYIMNLAVVD 89
 QY 120 QPRGYLMSLQTSLEFRRLGTRAAFEVLSSNVEGGAFOATRRGPGSTLRCRAPSSS 179
 DB 90 TFNDLEKRRKFKSLHKKRAIQHAYRLISQRRPAG---ISYRQEGLMREYK-PRMSA 144
 QY 180 ATTTLT-----TWGTSFQWQWCPACSCWMMQMCCL- 212
 DB 145 RERYLTFKALNONNTPLSLKDFYDIYEVALKWKAKKREHW-----FDELPTALLI 198
 QY 213 ---SVMTSSWGEFSTASSICTT---CW-----SCGSRSLPWACEGTCPPATCL 254
 DB 199 FKGINILVSKAFQYFMITLVAVANGWILVETFMKGGFESKHVFWST-----LVFL 251
 QY 255 T-----GSSPL-----SCWRP-----EMVGLSLMDTMRMLN-----LIYF 286
 DB 252 TIYGELEFLKAGLGPVEYELSSGWNLFDSYVVFALGILAL-----ALNMEPEFIYVL 306
 QY 287 R---FLRIIPSKPMAVAVASTYVLGVONKRAFGILLVYVYFAITIGINLFRGVIALPG 343
 DB 307 RPLQILRLFKLKERARNVLDITMFEELLPRMASLGLTLLIFYSFAIVGMEFFCGIYFPNCC 366
 QY 344 NSSLAP-----ANGSAPCGSEFOLEYWANNPDDEAALVLTLMNMMVNNQVFLD 393
 DB 367 NTSTYADAVRRNHTVGNRTV---VEEGYTLNPNFNDNLNLFVTLFELTVANNMYIME 422
 QY 394 AYRRYSQWMSKITYFLVLMVSSVIVWNLFLALILENLEFLHK 433
 DB 423 GVTSGTSHMSRLYFMTFYIVTMV-MTIIVATILEAFYR 461
 RESULT 8
 AAG75376
 ID AAG75376 standard; Protein: 594 AA.
 XX
 AC AAG75376;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:6140.
 XX
 KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.

XX OS Homo sapiens.
 XX PN WO200122920-A2.
 XX PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 DR WPI: 2001-235357/24.
 DR N-PSDB; AAH34781.
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11; Page 7588-7590; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAH7789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 594 AA;
 Query Match 13.0%; Score 342; DB 22; Length 594;
 Best Local Similarity 25.4%; Pred. No. 1.5e-24;
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;
 QY 60 YFQNPESLTSILVLTANNPDVMIAPSKRAVAIFETVFGSLMLNLTAAIIS 119
 DB 40 YFSTLSTNSIVSLFVLITLTFNPDVMPYSRNWSCVFETVYLSIELYIMNLAVVD 99
 QY 120 QPRGYLMSLQTSLEFRRLGTRAAFEVLSSNVEGGAFOATRRGPGSTLRCRAPSSS 179
 DB 100 TFNDLEKRRKFKSLHKKRAIQHAYRLISQRRPAG---ISYRQEGLMREYK-PRMSA 154
 QY 180 ATTTLT-----TWGTSFQWQWCPACSCWMMQMCCL- 212
 DB 155 RERYLTFKALNONNTPLSLKDFYDIYEVALKWKAKKREHW-----FDELPTALLI 208
 QY 213 ---SVMTSSWGEFSTASSICTT---CW-----SCGSRSLPWACEGTCPPATCL 254
 DB 209 FKGINILVSKAFQYFMITLVAVANGWILVETFMKGGFESKHVFWST-----LVFL 261
 QY 255 T-----GSSPL-----SCWRP-----EMVGLSLMDTMRMLN-----LIYF 286
 DB 262 TIYGELEFLKAGLGPVEYELSSGWNLFDSYVVFALGILAL-----ALNMEPEFIYVL 316
 QY 287 R---FLRIIPSKPMAVAVASTYVLGVONKRAFGILLVYVYFAITIGINLFRGVIALPG 343
 DB 317 RPLQILRLFKLKERARNVLDITMFEELLPRMASLGLTLLIFYSFAIVGMEFFCGIYFPNCC 376

YY	344	NSSLAP-----ANGSAPCSFEQLEVMANNDEFAALATLMLAVNNMQVFLD	393
Dd	377	NFTSVADAYARRRNMHTVGNRIV---VEEGYTLNNEFDNIISFYLIFELTVNNMYTIME	432
OY	394	AYRRYSQPSWKIYFYLMVLWSSVIWNVDLALLILENLHK	433
Dd	433	GVTSGTSHMSRLYFMTEFYITVMV-METIIAFILEAFVER	471
RESULT 9			
ID	AAB60097		
AC	AAB60097;	standard; Protein: 748 AA.	
Dt	28-MAR-2001	(first entry)	
XX			
DE	Human transport protein TPPT-17.		
KM	Human; transport protein; TPPT; transport disorder; metabolic disorder;		
KW	neurological disorder; cardiovascular disorder; reproductive disorder;		
KM	immune disorder; cancer.		
OS	Homo sapiens.		
PN	WO200078953-A2.		
PD	28-DEC-2000.		
PF	16-JUN-2000; 200OWO-US16668.		
PR	17-JUN-1999; 99US-0139923.		
PR	10-AUG-1999; 99US-0148177.		
PR	18-AUG-1999; 99US-0149357.		
PR	28-OCT-1999; 99US-0162287.		
PA	(INCY-) INCYTE GENOMICS INC.		
PI	Lal P, Yang J, Yue H, Hillman JL, Tang YT, Bandman O, Burford N;		
PL	Baughn MR, Azimzai Y, Lu DAM, Au-Young J, Patterson C;		
DR	WPI: 2001-041424/05.		
DR	N-PSDB: AAF27117.		
XX			
PT	Isolated polypeptide with a human transport protein sequence is useful		
PT	for the diagnosis, prevention and treatment of disorders associated		
PT	with the immune, reproductive and cardiovascular systems -		
PS	Claim 2; Page 118-120; 165pp; English.		
CC	The present invention provides the protein and coding sequences for 43		
CC	novel human transport proteins (designated TPPTs). These can be used in		
CC	the diagnosis and treatment of transport, metabolic, neurological,		
CC	reproductive, cardiovascular and immune disorders, and cell proliferative		
CC	disorders such as cancer.		
XX			
SQ	Sequence 748 AA:		
Query Match	13.0%; Score 342; DB 22; Length 748;		
Best Local Similarity	25.4%; Pred. No. 2.1e-24;		
Matches 117; Conservative	71; Mismatches 158; Indels 114; Gaps 17		
OY	60	YQNLPESLTSLVLTITANNPDVMIIPAKSKRAVAIFEIVTYIGSLIMNLTIAIYS	119
Dd	194	VSTLENISNTLSLITANFPDWMPSYSRNPWSCVFETIVISTIELYITMNLAVVD	253
OY	120	OPRGYLMKSIGTSLEFRRLGTRAAEFVLSMGEGAFPQATRRGPSTLRFCRAPSSSS	179
Dd	254	TINDIEKRFRKLLHLKRTAIQHAYLLISQRPPAG---ISRQREGMLRRFYK-PRMSA	308
OY	180	ATTTLT-----TWGTSSWGQTWCPCPACSCWMQMCCCL-	212

Dd		309	RERITTEFALMÖNNPTLLSLKDFDIYEVAAKKAKKNNEHW-----PDELPRALLI	362
Oy		213	----SVMTSMGEFTASLCTT---CW-----SCCSRLFPACSGTCPTPATCL	254
Dd		363	EKGINILTKSKAFQFYEMLYVAANGVILVETFMILKCGNFFSKIVPSWY-----LVFL	415
Oy		255	T-----GSSPL-----SCWRP-----ENYGILSDMDMTMLNM-----LIVE	286
Dd		416	TIYGYELFKAVAGLPVYVLSSGNKLDPFSVTAYAFGLLAL-----ALMNEPFYIVL	470
Oy		287	R--FLRIIPSMKPMAVVASTVLGIYNOMRAEGSILVVYVVEAIIIGINLFRGVIALPG	343
Dd		471	RPLQLRLFLKLERARNLDIMFELEPPMASLGILLTFIFYSFATVGMEFFCGIVFPNC	530
Oy		344	NSSLAP-----ANGSAPCGSFEDELEYMANPDFAALVTLNLMVNVMVOYEFD	393
Dd		531	NTSTVADAYRMRNRHTVGRITY-----VEGGYYLNNFDNIILNSFYTLRELTIVNNMYIME	586
Oy		394	AYRRYSGPSKIYEFYLMVLVSSVIYVNLFLAILLENLHK	433
Dd		587	GVTQSOTSHMSRLRYEMTFEYIVAMV-MRTIVAFILLEAFVER	625
Db				
RESULT	10		.	
AAG77820	ID	AAG77820	standard; Protein; 816 AA.	
XX	AC	AAG77820;		
XX	DT	05-DEC-2001	(first entry)	
XX	DE		Human ion channel 23927 protein (IC33927).	
XX	KX			
KW	KM	IC33927; human; ion channel 23927; gene therapy; screening assay;		
KW	KM	predictive medicine; pharmacogenetics; pain disorder;		
KW	KM	central nervous system disorder; ion transport; ion conductance;		
KW	KM	membrane bound protein; membrane excitability; membrane polarisation;		
KW	KM	synaptic transduction; pain signaling; cell activation; cell growth;		
KW	KM	cell proliferation; cell differentiation; cell migration;		
KW	KM	muscle contraction.		
XX	OS	Homo sapiens.		
XX	PH			
PH	Key	Location/Qualifiers		
FT	FT	114..128	/note= "Transmembrane domain 1"	
FT	FT	146..168	/note= "Transmembrane domain 2"	
FT	FT	178..195	/note= "Transmembrane domain 3"	
FT	FT	199..210	/note= "Transmembrane domain 4"	
FT	FT	233..254	/note= "Transmembrane domain 5"	
FT	FT	269..287	/note= "Pore domain: an overall hydrophobic domain"	
FT	FT	298..320	/note= "Transmembrane domain 6"	
FT	FT	443..465	/note= "Transmembrane domain 7"	
FT	FT	482..502	/note= "Transmembrane domain 8"	
FT	FT	510..532	/note= "Transmembrane domain 9"	
FT	FT	539..554	/note= "Transmembrane domain 10"	
FT	FT	570..594	/note= "Transmembrane domain 11"	
FT	FT	637..653	/note= "Pore domain: an overall hydrophobic domain"	
FT	FT	666..687	/note= "Transmembrane domain 12"	
XX				

PN W0200164881-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US06530.
 XX
 PR 29-FEB-2000; 2000US-0185938.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ, Silos-santiago I;
 XX
 DR WPI: 2001-570694/64.
 DR N-PSDB; AAH78802, AAH78803.
 XX
 PT Isolated ion channel polypeptide IC23927 useful in screening assays and
 PT treatment of disorders, e.g., central nervous system disorders and pain
 PT disorders
 XX
 PS Claim 14; Fig 1; 142pp; English.
 XX
 CC The present sequence represents the human ion channel 23927 (IC23927)
 CC protein, which is claimed in the invention. The ion channel family of
 CC proteins is a large family of membrane bound proteins responsible for a
 CC wide range of transport and signalling functions in cells. The invention
 CC comprises IC23927 proteins and nucleic acids. The IC23927 nucleic acids
 CC and proteins may be used in screening assays, predictive medicine (e.g.,
 CC diagnostic assays and pharmacogenetics) and treatment of disorders
 CC characterised by insufficient production of IC23927 (e.g., central nervous
 CC system disorders, pain disorders, or disorders of cellular growth,
 CC differentiation or migration). The IC23927 nucleic acids and proteins are
 CC also useful as targets for developing modulating agents to regulate a
 CC variety of cellular processes, such as: ion transport (e.g., ion
 CC conductance); membrane excitability and/or polarisation; synaptic
 CC transduction (e.g., pain signalling); cell activation; and muscle contraction.
 CC cell growth; cell differentiation; cell migration and muscle contraction.
 CC Administration of a modulator of IC23927 (especially by gene therapy) may
 CC be used to treat pain or a pain disorder.
 XX
 SQ Sequence 816 AA;
 Query Match 13.0%; Score 342; DB 22; Length 816;
 Best Local Similarity 25.4%; Pred. No. 2.3e-24;
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;
 QY 60 YFONLPESLTSVLVLTANNPDVMPAYSKNRAIAFFIVFYIGSLFTMLNLTATIS 119
 DB 262 YFSTLENSIVSLFVLTTANFPDVMPSYSRNPMSCVFIVYISTELFTMLNLTAVFD 321
 QY 120 QFNGYLMKSLQTSIFRRRLGTRAFAEVLSSMVBEGGAFPOATRGRGPTSLRCPAPSSSS 179
 DB 322 TFMDIEKRRKKSLLHRRRAIOHAYRLISQRRPAG---ISYRQFGLMRFYK-PRMSA 376
 QY 180 ATTTLT-----TWGTSPPQWTCOPFACSCMCMQCCLT- 212
 DB 377 RERYLTFKALNQNNTPLSLKDFYDIYEAALMKAKKNEHM-----FDELPRALLI 430
 QY 213 -----SWTSSWGFSSTASLCTT---CW-----SCCSRLPWACGTCPTPATCL 254
 DB 431 FKGINILVSKAFQYFMYLVAANGVWIIIVETFMKGNFNSKHVPSY-----LVFL 483
 QY 255 T-----GSSPL-----SCWRP-----EMVGLSLMDMRLNM-----LIVF 286
 DB 484 TIYGVLEFLKAVAGLGEVEYISSGMNLFDSVTFAPFLGLTAL-----ALMMEPFYFIVL 538
 QY 287 R---FLRIIPSMKPAVVAIVAGLVQNMRAFGILVVVVYVAIGINLFRGVIALPG 343
 DB 539 RPLQTLRLFLKERYRNVDLTMEPLPRMASHGLTILIFYSRAIYGMFPCIVAPNCC 598
 QY 344 NSSLAP-----ANSAPGCSFEQLEIYMANNFDDPAALVLTMLNIVVNNMOVFD 393
 DB 599 NISTVADAYRMNRHVTGNRTY---VEEGYIYNLNDNINLSHVTLELTVANNVYIME 654

QY 394 AYRRYSGPWSKIFYVLMMLVSSVIMVNLFLALILENFKL 433
 DB 655 GVTSTQSHWSRLYFMFTFIVTMV-MTIIVAFLEAFVR 693
 RESULT 11
 ID AAM23901
 AC AAM23901 standard; Protein; 520 AA.
 AC AAM23901;
 DT 12-OCT-2001 (first entry)
 DE Rat Est encoded protein SEQ ID NO: 1426.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 OS Rattus norvegicus.
 XX
 PN W0200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX
 DR WPI: 2001-476164/51.
 DR N-PSDB; AAH98560.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX
 PS Claim 20; Page 992-993; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 520 AA;
 Query Match 12.8%; Score 336; DB 22; Length 520;
 Best Local Similarity 25.0%; Pred. No. 4.9e-24;
 Matches 115; Conservative 72; Mismatches 159; Indels 114; Gaps 17;
 QY 60 YFONLPESLTSVLVLTANNPDVMPAYSKNRAIAFFIVFYIGSLFTMLNLTATIS 119
 DB 30 YFSTLENSIVSLFVLTTANFPDVMPSYSRNPMSCVFIVYISTELFTMLNLTAVFD 89
 QY 120 QFNGYLMKSLQTSIFRRRLGTRAFAEVLSSMVBEGGAFPOATRGRGPTSLRCPAPSSSS 179
 DB 90 TFMDIEKRRKKSLLHRRRAIOHAYRLISQRRPAG---ISYRQFGLMRFYK-PRMSA 144
 QY 180 ATTTLT-----TWGTSPPQWTCOPFACSCMCMQCCLT- 212
 DB 145 RERYLTFKALNQNNTPLSLKDFYDIYEAALMKAKKNEHWD-----ELPRALLI 198

QY 213 ----SYMTSSGGEFSTASSICTT---CW-----SCGSRSLPMACEGCTPTPACCL 254
 DB 199 FGINILVAKAKAFQYEMYLVAVNGVILVETFMKLGKGFESKHWPMST-----LVFL 251
 QY 255 T-----GSSPL-----SCWRP-----EMVGLLSMDTMRMLN-----LVIE 286
 DB 252 TIYGEVLEFLKAVAGLGFVEILSSGWNLFDPSSVYVFAFLGIAL-----ALNMEPEFFIYVL 306
 QY 287 R--FLRIIPSKPMVAVASTVLGIQVONNRAFGILIVVYVFAITIGLNGRGTVALDG 343
 DB 307 RPLQLRLFKLKERVRNVLDTMFELLPRMASLGLTLIFVYSPFAIVGMFEFCGIVFPNCC 366
 QY 344 NSSLAP-----ANGSAPCGSPEDQLEVMANNFDDPAALVTLMLNVMYNNVOVFLD 393
 DB 367 NSTVADAVRMRNHTVGNRTV---VEEGYTLNNDNLNSFVTLFELTVNNMYITME 422
 QY 394 AYRRYSQPMSKIYFVLMWLVSSYIWNLFALILENLELHK 433
 DB 423 CVTSQTSNHSRLYEMTFYIATMNV-WTIIVAFILFAFVR 461
 RESULT 12
 AAM25607
 ID AAM25607 standard; Protein; 395 AA.
 XX
 AC AAM25607;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:1122.
 XX
 KW Human: Cancer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antidiabetic; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antilipidemic; haemostatic; vulnary; antitumor; osteopathic; eczema;
 KW dermatological; antiallergic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antinaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 KW
 XX Homo sapiens.
 OS
 XX MO20015345-A2.
 PN
 XX 26-JUL-2001.
 PD
 XX 22-DEC-2000; 2000MO-US35017.
 PF
 XX 23-DEC-1999; 99US-0471275.
 PR 21-JAN-2000; 2000US-048725.
 PR 25-APR-2000; 2000US-0552317.
 XX
 PA (HYSE-) HYSEO INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI: 2001-457603/49.
 DR N-PSDB; AAH99548.
 XX
 PT Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX
 XX Claim 20; Page 232; 1217p; English.
 XX
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and

CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antilipidemic; antitumor; osteopathic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 SQ Sequence 395 AA;
 XX
 Query Match 7.9%; Score 208; DB 22; Length 395;
 Best Local Similarity 29.3%; Pred. No. 1.2e-11;
 Matches 54; Conservative 39; Mismatches 63; Indels 28; Gaps 6;
 QY 268 VGLSLMDTMRMLN-----LIVER---FLRIIPSKPMVAVASTVLGIQVONNRAFGIL 319
 DB 99 LGILAL-----ALNMEPEFFIYVLRPLQLRLFKLKERVRNVLDTMFELLPRMASLGLTL 153
 QY 320 VVYVYFAITIGILNFRGYVALPGNSSLAP-----ANGSAPCGSPEDQLEVMANNF 369
 DB 154 LIFYSPFIVMEFCGIVFPNCCNTSTVADAVRMRNHTVGNRTV---VEEGYTLNND 209
 QY 370 DDEFAALVTINMLVNNVOVFLDAYSRRYSGPMSKIYFVLMWLVSSYIWNLFALILEN 429
 DB 210 DNLNSFVTLFELTVNNMYITMEGYSQTSNHSRLYEMTFYIATMNV-WTIIVAFILFA 268
 QY 430 FLHK 433
 DB 269 FVFR 272
 RESULT 13
 AAR33545
 ID AAR33545 standard; Protein; 2161 AA.
 XX
 AC AAR33545;
 XX
 DT 30-JUN-1993 (first entry)
 XX
 DE Sequence of the alpha 1D human calcium channel subunit.
 XX
 KW Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW Lambert Eaton syndrome.
 KW
 XX Homo sapiens.
 OS
 XX MO9304083-A.
 PN
 XX 04-MAR-1993.
 PD
 XX 14-AUG-1992; 92MO-US06903.
 PF
 XX 15-AUG-1991; 91US-0745206.
 PR 10-APR-1992; 92US-0868354.
 XX
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 PI Williams ME;
 XX
 XX WPI: 1993-093936/11.

DR N-PSDB; AA037811.

XX DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and
PT diagnosing Lambert Eaton syndrome

XX Disclosure: Page 93-101; 150pp; English.

XX The alpha 1D subunit cDNA was isolated using fragments of the
CC rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a
CC probe to screen a cDNA library of a human neuroblastoma cell line,
CC IMR32, to obtain clone alpha 1.36. This clone was used as a probe to
CC screen additional IMR32 cell cDNA libraries to obtain overlapping
CC clones which were then employed for screening until a sufficient
CC series of clones to span the length of the nucleotide sequence
CC encoding the human alpha 1D subunit were obtained, see AA037811.
CC AA037812 provides the sequence of an alternative exon encoding the 156
CC transmembrane domain of the alpha 1D subunit. The alpha 1D protein
CC has a calculated Mr of 245,163.

XX Sequence 2161 AA;

Query Match 7.4%; Score 195; DB 14; Length 2161;

Best Local Similarity 18.7%; Pred. No. 2.2e-09; Mismatches 95; Conservative 80; Indels 176; Gaps 20;

```

QY 12 CRLGGMMVPTGWNVGLSLMGDPVPMSCRFCSQDDGDRRLTYFQNLPESTSL 71
DB 333 CR--SGWVAPNGI-----TNDNFAFALTY 357
QY 72 LVLLTTANPNPVMIPAYSKNRAVA-----IFFIVYIGSLFNLMLTAITYSQFGYLM 136
DB 358 FQCTIMEGWTIVL---YWNDAWGFEPLWYFVSLVIFGSPFVNLVGLSGEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAAFEVLSSMWG-----EGG-----APF----- 158
DB 415 KAKARGDFQKLRKQLEEDLKGYLDWITQAEIDIPNEEGEGEGEKRTSMPTSETSY 474
QY 159 -----QATRRGPSTSLRCRAPSSSATTTLTTWGTSSPWOPTWCPACSMC----- 204
DB 475 NTEVSGEGENKCCGSL--COAISKSK-----LSRRMRMRNFRNTRCRAAVKSY 523
QY 205 --WMOMCCL-LSVMTSS-----WGF--STASSLCTTCMSC-----GSRSLP--- 240
DB 524 TFYWLIVLVLFNTLITSSHYNOPDMVIOIDIANKVLALFTCEMLVKMYSLGQAYF 583
QY 241 -----WACEGTCPTPATCLTGSSPLSCWRPEWGLSLMDMTRLMLMLIVPRFLR 290
DB 584 VSLFNRFDFVYCGITETILVELEIMSPLG-----ISVFRCVRLLR 625
QY 291 IIPSMKPMVAVSTVLGVQNMRAFGIILVYV---YFAIIGINLFRGVIALPQNSSL 347
DB 626 IFNVTHMTSLSLVSLASMSKSLASLTLFLFTIFSLGMOFLGFKF----- 676
QY 348 APANGSAPGSEFQLEFYMANNFDEFAALVLTMLVAVVNMWQ-VFLDAVRAVSGPMK-- 404
DB 677 -----NFEDETQKSTFDNFPQALLTFQILITGEDMNAVATDGMATGPGSSGM 726
QY 405 ---LYFVLMVAVSVYVWVLFALILLEN 429
DB 727 IVCITFILLFCGNVTLNLVFLAIADVN 754

```

RESULT 14

AA071001

AA071001 standard: Protein; 2161 AA.

AA071001;

30-NOV-1995 (first entry)

Human neuronal calcium channel subunit alpha 1D.

KW Calcium channel subunit; antagonist; agonist; diagnosis;

KW Lambert Eaton Syndrome.

XX Homo sapiens.

XX W09504822-A.

XX 16-FEB-1995.

XX 11-AUG-1994; 94WO-US09230.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Ellis SB, Gillespie A, Harpold MW, McCue AF, Williams ME;

XX WPI; 1995-090900/12.

XX N-PSDB; AA084653.

PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists

PS Disclosure: Page 116-126; 285pp; English.

The alpha 1D subunit cDNA has been isolated using fragments of the
CC rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a
CC probe to screen a cDNA library of human neuroblastoma cell line
CC IMR32, to obtain clone alpha 1.36. This clone was used as a probe to
CC screen additional IMR32 cell cDNA libraries to obtain overlapping
CC clones, which were then employed for screening until a sufficient
CC series of clones to span the length of the nt sequence encoding the
CC human alpha 1D subunit was obtd. Full-length clones were then
CC constructed by ligating partial clones. AA084653 shows the nt sequence
CC of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has
CC a calculated Mr of 245,163. It contains four putative internal
CC repeated sequence regions which represent 24 putative transmembrane
CC segments. It mediates DHP-sensitive high-voltage, long-lasting
CC calcium channel activity.

XX Sequence 2161 AA;

Query Match 7.2%; Score 190; DB 16; Length 2161;

Best Local Similarity 18.5%; Pred. No. 6.7e-09; Mismatches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

```

QY 12 CRLGGMMVPTGWNVGLSLMGDPVPMSCRFCSQDDGDRRLTYFQNLPESTSL 71
DB 333 CR--SGWVAPNGI-----TNDNFAFALTY 357
QY 72 LVLLTTANPNPVMIPAYSKNRAVA-----IFFIVYIGSLFNLMLTAITYSQFGYLM 136
DB 358 FQCTIMEGWTIVL---YWNDAWGFEPLWYFVSLVIFGSPFVNLVGLSGEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAAFEVLSSMWG-----EGG-----APF----- 158
DB 415 KAKARGDFQKLRKQLEEDLKGYLDWITQAEIDIPNEEGEGEGEKRTSMPTSETSY 474
QY 159 -----QATRRGPSTSLRCRAPSSSATTTLTTWGTSSPWOPTWCPF-----AC 201
DB 475 NTEVSGEGENKCCGSL--COAISKSK-----LSRRMRMRNFRNTRCRAAVKSY 523
QY 202 SMCWMOMCCL-LSVMTSS-----WGF--STASSLCTTCMSC-----GSRSLP--- 240
DB 524 TFYWLIVLVLFNTLITSSHYNOPDMVIOIDIANKVLALFTCEMLVKMYSLGQAYF 583
QY 241 -----WACEGTCPTPATCLTGSSPLSCWRPEWGLSLMDMTRLMLMLIVPRFLR 290
DB 584 VSLFNRFDFVYCGITETILVELEIMSPLG-----ISVFRCVRLLR 625
QY 291 IIPSMKPMVAVSTVLGVQNMRAFGIILVYV---YFAIIGINLFRGVIALPQNSSL 347

```

```

Db      626  IFKVTYRHTSISNLYVASILSMKSIASILLLEFIITFISLGMQFGKF----- 676
QY      348  APANGSAPCGSEFQLEYWANNFDEFAALVTLNMLAVNNMO--VFLDAYRRYSGPMSK-- 404
Db      677  -----NFDQTKRSTFDNFPQALLTVFQILTGEDMNAVMYGIAYGSPSSSGM 726
QY      405  ---TYFVLMVLVSVIWNVLFALILEN 429
Db      727  IVCIYFIILFCGNVILLNVFLATAVDN 754

RESULT 15
AAR71002
ID      AAR71002 standard; Protein; 2161 AA.
XX      AAR71002;
XX      30-NOV-1995 (first entry)
DE      Human neuronal calcium channel subunit alpha 1D including alternative.
DE      exon encoding the I56 transmembrane domain.
XX      Calcium channel subunit; antagonist; agonist; diagnosis;
XX      Lambert Eaton Syndrome.
XX      Homo sapiens.
OS
FH      Key Location/Qualifiers
FT      Misc-difference 373..406
FT      /label= encoded by alternative exon
XX      W09504822-A.
XX      16-FEB-1995.
XX      11-AUG-1994; 94WO-US09230.
XX      11-AUG-1993; 93US-0105536.
XX      05-NOV-1993; 93US-0149097.
XX      (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX      Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME.
XX      WPI; 1995-090900/12.
XX      N-PSDB; AA084654.
XX      DNA encoding human calcium channel sub-unit(s) - used for
XX      developing prods. for studying calcium channels, e.g. for
XX      obtaining agonists and antagonists
XX      Disclosure; Page 126-127; 285pp; English.
XX
XX      The alpha 1D subunit cDNA has been isolated using fragments of the
XX      rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a
XX      probe to screen a cDNA library of human neuroblastoma cell line
XX      IMR32, to obtain clone alpha1.36. This clone was used as a probe to
XX      screen additional IMR32 cell cDNA libraries to obtain overlapping
XX      clones, which were then employed for screening until a sufficient
XX      series of clones to span the length of the nt sequence encoding the
XX      human alpha 1D subunit was obtained. Full-length clones were then
XX      constructed by ligating partial clones. AA084653 shows the nt sequence
XX      of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has
XX      a calculated Mr of 245,163. It contains four putative internal
XX      repeated sequence regions which represent 24 putative transmembrane
XX      segments. It mediates DHP-sensitive high-voltage, long-lasting
XX      calcium channel activity. AA084654 shows an alternative exon encoding
XX      the I56 transmembrane domain. The difference occurs in AAs 373-
XX      406.
XX      Sequence 2161 AA;
SQ

```

```

Query Match      7.2%; Score 190; DB 16; Length 2161;
Best Local Similarity 18.5%; Pred. No. 6.7e-09;
Matches 94; Conservative 83; Mismatches 155; Indels 176; Gaps 20;

QY      12  CRIGGWMVPTGWRKGLSLMGDBVYVWSCRFCSDDDGDRRLVYFQALPSPSLSL 71
Db      333  CR--SGWVGPNGI-----TFNDFAFAMLTIV 357
QY      72  LVLLTANNPDVWIPAYSKNRAVA-----IFFIVTIGSLFLMNLTAIISQFQYLM 126
Db      358  FQCTITWEGMTDLV---YWNDAIGHEWMPVYFVSLIIISFFVLMNLVGLVSGERSKERE 414
QY      127  KSLQTSIFRRRLGTGRAFEVLSSWVG-----EGG-----AP----- 158
Db      415  KAKARQDFQKLRKQOLEEDLKGYLDWITQAEIDPENEEGEGEKRTSMPTSETSEV 474
QY      159  -----QATRRGPSTSLRCPAPSSSATTTLTWTGTSPPQWTCPF-----AC 201
Db      475  NTEVSGEGENKCCGSL--COAISKSK-----LSRRRRNRNFRNRRCRAAVKSV 523
QY      202  SMCMMQMCCLLSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP--- 240
Db      524  TFYWLIVLVFLMTLITLISSEHYNQPDMLQIQDIANKVLLALETCMLVKMYSLGIQAYF 583
QY      241  -----WACEGTCPTPATCTLTGSSPLSCWRPENVGLSLMDTRMLNMLIVRFRIR 290
Db      584  VSLFNRFDCEVVGCIETILLVEILMSPLG-----ISVRCYRLIR 625
QY      291  IIPSMKPMAVASVYGLVONMRAFGIIVVY---VFPAIIGINLFRGVYVALPQNSSL 347
Db      626  IFKVTYRHTSISNLYVASILSMKSIASILLLEFIITFISLGMQFGKF----- 676
QY      348  APANGSAPCGSEFQLEYWANNFDEFAALVTLNMLAVNNMO--VFLDAYRRYSGPMSK-- 404
Db      677  -----NFDQTKRSTFDNFPQALLTVFQILTGEDMNAVMYGIAYGSPSSSGM 726
QY      405  ---TYFVLMVLVSVIWNVLFALILEN 429
Db      727  IVCIYFIILFCGNVILLNVFLATAVDN 754

```

Search completed: October 8, 2002, 10:02:41
 Job time : 62 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:02:16 ; Search time 24 Seconds

(without alignments)
493.601 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634
Sequence: 1 MSSACWEATGRCRLGCGMNV.....PCDELTERTLSQHPHLICLR 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	192	7.3	1872	6	5386025-6
2	190	7.2	2161	1	US-07-745-206A-2
3	190	7.2	2161	1	US-08-455-543A-49
4	190	7.2	2161	1	US-08-455-543A-51
5	190	7.2	2161	2	US-08-223-305C-49
6	190	7.2	2161	2	US-08-223-305C-51
7	190	7.2	2161	2	US-08-311-363-2
8	189	7.2	1873	1	US-08-336-257A-7
9	186	7.1	1873	1	US-08-435-625B-4
10	185.5	7.0	1754	1	US-07-745-206A-13
11	185.5	7.0	1754	2	US-08-311-363-13
12	178.5	6.8	1968	1	US-08-455-543A-45
13	178.5	6.8	1968	2	US-08-223-305C-45
14	175.5	6.7	2237	1	US-08-455-543A-48
15	175.5	6.7	2237	2	US-08-223-305C-48
16	175.5	6.7	2237	4	US-09-268-163-8
17	175.5	6.7	2237	3	US-08-713-118-2
18	175.5	6.7	2237	4	US-09-452-007-2
19	175.5	6.7	2339	1	US-08-455-543A-47
20	175.5	6.7	2339	2	US-08-223-305C-47
21	175.5	6.7	2339	4	US-09-268-163-6
22	175.5	6.7	2343	4	US-09-268-163-4
23	174.5	6.6	823	1	US-07-745-206A-15
24	174.5	6.6	823	2	US-08-311-363-15
25	171	6.5	2273	4	US-09-426-998-5
26	170.5	6.5	1835	4	US-09-404-650-5
27	169.5	6.4	2353	4	US-08-984-709A-50

28	168.5	6.4	2265	2	US-08-149-097D-36	Sequence 36, Appl
29	168.5	6.4	2509	2	US-08-149-097D-35	Sequence 35, Appl
30	168	6.4	2336	4	US-09-268-163-10	Sequence 10, Appl
31	167.5	6.4	2175	4	US-09-404-650-2	Sequence 2, Appl
32	167.5	6.4	2188	4	US-09-404-650-4	Sequence 4, Appl
33	163.5	6.2	1956	4	US-08-843-417-10	Sequence 10, Appl
34	160.5	6.1	2104	2	US-08-808-793-4	Sequence 4, Appl
35	160.5	6.1	2104	3	US-08-772-512A-4	Sequence 4, Appl
36	160.5	6.1	2105	3	US-08-808-793-3	Sequence 3, Appl
37	160.5	6.1	2105	3	US-08-772-512A-3	Sequence 3, Appl
38	156	5.9	813	3	US-08-836-325-8	Sequence 8, Appl
39	155.5	5.9	1968	1	US-07-745-206A-7	Sequence 7, Appl
40	155.5	5.9	1968	2	US-08-311-363-7	Sequence 7, Appl
41	155.5	5.9	2516	3	US-08-374-077C-2	Sequence 2, Appl
42	155.5	5.9	2516	4	US-08-895-590-2	Sequence 4, Appl
43	154.5	5.9	2016	4	US-09-634-920-4	Sequence 4, Appl
44	151.5	5.8	1984	3	US-08-836-325-10	Sequence 10, Appl
45	150.5	5.7	1011	3	US-08-836-325-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
5386025-6
Patent No. 5386025
; APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
; M. CAMPBELL, KEVIN P.
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,384
; FILING DATE: 20-FEB-1990
; SEQ ID NO: 6
; LENGTH: 1872
5386025-6

Query Match 7.3%; Score 192; DB 6; Length 1872;
Best Local Similarity 18.3%; Pred. No. 9.2e-10;

Matches 95; Conservative 81; Mismatches 165; Indels 178; Gaps 19;

QY	58	LTFFONLPEESITSLVLLTTANPDVMTAYSKNRYA-----IFFYFVIGSLFMTL 112	
DB	272	ITHFDNFGSMFTVYQCITMEGWTDVL---YTVDAIGNEMPIYFTLLIGSFILNL 328	
QY	113	LTATTSYSPRGTLKMSLQTSIFRRRLGTRAFEVLSSWVG----- 152	
DB	329	VIGVLSGFTKERERAKSRGTFOKIREKOOLEEDLRGYMSWITOGEDYEDLREGKLSL 388	
QY	153	-EGAFPOATR--RQPSLSRCRAPSSSATLTLLTWTGSSPWQTM---CPFACS--- 202	
DB	389	EEGSDTSLYEIRGLNKTIQFIR-----HWRONRYFRMKCHDLVK 430	
QY	203	---NCWQMC-----CLLSVYT-----SSWGFSTAS 225	
DB	431	SRVEFWLILVALNTLSIASEHNQPLMLTODIANRVLLSFTEMLLMKYGGLRQ 490	
QY	226	SLCT-----TQWSSCSRSLP--WAGEGCPPTATLTSSPLSCRPREMGILSLMDTRM 279	
DB	491	YFMSTFNRFDCFWVCSGLLELLVESGAMP---LGISVLR----- 529	
QY	280	LNMILVERFLRIISMKPMAYVASTVLGLVQNMRAFGIIVVVY---YFAIGINLFRG 336	
DB	530	-----IRLRLFKITTYWTSLSLVASLNTSISLILLLFLFIITRALLGMQLFG 583	
QY	337	VIVALLPGNSLAPANGSAPCGSFQLEFWANFNDFEAAALVTLMNVVNNW--QVFLDAY 395	
DB	584	RY-----DFEDTEVRNSNEDNFPOALISYFOVLTGEGDMSSVMYNGI 624	
QY	396	RRYSGPWSK-----YFVLMWLVSSVIMVNDLFLALIENTLH-----TWDRSHL 440	
DB	625	MAYGSPSPVGLVGLVITYITIIIFVCGNITLLNVFTLAIIVANDLAEBSLTSQAKAAEERKR 684	

QY 441 OPLAGPEATYMTVELLFRDLEPEGEDELTERLSQHP 479
DB 685 KMSRGLPDKT-----EERKSVAKKLEQRP 709

RESULT 2

US-07-745-206A-2
Sequence 2, Application US/07745206A
Patent No. 5429921
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-2

Query Match 7.28; Score 190; DB 1; Length 2161;
Best Local Similarity 18.58; Pred. No. 1.8e-09;
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGMMVPTGNVRLGELSLMGDPVYPWSCRFCGQDGDORRLTYFQNLPESTLSL 71
DB 333 CR--SGWGRNGT-----TNDNFAPMLLV 357
QY 72 LVLLTTANPDVMIPTASKRNYA-----IFETVYVIGSLFLMNLTAITYSQFQYLM 126
DB 358 FQCTMEGMDVY--YWMNDAMGELPWPVYFSLVIFSGFEVLNLVLGYLSEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAFEVLSNVG-----EGG-----AFP----- 158
DB 415 KAKARGDOKRERKQOLEEDKGYLDWITQAEIDDPENEEGGEGEGRNTSMPTSESEV 474
QY 159 -----QATRRGPSTLRFCAFPSSSSATTTLTWTGTSFQWQWCP-----AC 201
DB 475 NTEVNSGEGENRGCGSL--CQATSKSK-----LSRRWRMNFRNRRCRAAVKSV 523
QY 202 SWCMQKQCL--LSVMTSS-----WGF-----STASSLCTTCWGC-----CSNLP--- 240
DB 524 TFYMLVIVLVLNLTLSSEHYNQPDMLTQIDTANKVLLALFTCEMLVKYSLGLQAYF 583
QY 241 -----WACGTCPTPATCTLGSSSPLSCWBPENVAGLLSLMDMTMLNMLIVFQFLR 290

DB 584 VSLFNRDCEVYCGGITEITLVELEINSPLG-----ISVRCVRLR 625
QY 291 IIPSMKPAVAVSTVLGYONMRAFGILVVY---YFAIIGINIFRGYVALPQNSSL 347
DB 626 IFKTRHWTSLSNVSLNLSMKSIAISLILLLFLFIIFSLMQLFQKFE----- 676
QY 348 APANGSAPCGSFEQLEYWANNFDDFAALVTLNMLVYNNWQ--VFLDATRYGSPMS-- 404
DB 677 -----NFDETQTRSTFDNFPOALLTVQILTGEDMNAVMYDGIAYGSPSSSGM 726
QY 405 ---YFVIMLVSSVIVWNLFLALLEN 429
DB 727 IVCIFIFLFCGNVILNVLALAVDN 754

RESULT 3

US-08-455-543A-49
Sequence 49, Application US/0845543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-455-543A-49

Query Match 7.2%; Score 190; DB 1; Length 2161;
 Best Local Similarity 18.5%; Pred. No. 1.8e-09;
 Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGWVPTGWRGLSLMGDVPVWSCRFCSSQDDGDRRLTYFQNLPESTLSL 71
 DB 333 CR--SGWVGPNCGI-----TFDNFAFAMLTIV 357
 QY 72 LVLLTANNPDVMIPIAYSKRAYA-----IFFTVTVIGSLFLMNLTAITYSQFGYLM 126
 DB 358 FOCITMEGTDLV---YWNDAIGWEMPVYFVSLIIGSFVLNLVGLSGEFSKERE 414
 QY 127 KSLQTSLFRRLGTAAFEVLSSWVG-----EGG-----APF----- 158
 DB 415 KAKARGDFQKLRKQOLEEDLKGIDWITQAEIDIPENEEGEGEGRKNTSMPTSETSV 474
 QY 159 -----QATRRGPSTSLRCPAPSSSATTTLTWTGSSPWOTWCF-----AC 201
 DB 475 NTENVSGEGENRCGCSL--CQAISSK-----LSRRMRMRNRRRCRAAVKSV 523
 QY 202 SMCWMOMCL-LSVMTSS-----WGF-----STASSLCTTQMSC-----CGRSLP--- 240
 DB 524 TTYMLVIVLFTLITISEHYNQDPWLQIODIANKVLLALFTCEMLYKMSLGLQAYF 583
 QY 241 -----WACEGTCPATCLTSSPSLSCWRPEMVGLLSIMDTRMLNLIVRFLR 290
 DB 584 VSLFNRDFCVVCGGITETILVLELMSPLG-----ISVRCLRLLR 625
 QY 291 ITPSKPMVAVSTYGLVQNNRAGGILVYV---YPAIIGINLFRGVYALPQNSSI 347
 DB 626 IFKVTIRHMTSLNVLASLNSKMSIASILLFLFIIFSLGMQIFGKFE----- 676
 QY 348 APANSGAPCGFEQLEYMANNDDEFAALVTLMLNLVAVNNQ-VFLDARRRSGPSK-- 404
 DB 677 -----NDETQTKRSTFDNFPQALLTFVQILGEDMNAVMYDGIAMVGGPSSGM 726
 QY 405 ---IYFVLMVLVSVIWNLFALILLEN 429
 DB 727 IVCIVFILLFIGGNVILLNVLAIANDN 754

RESULT 4
 US-08-455-543A-51
 Sequence 51, Application US/08455543A
 Patent No. 5792846
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA

ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-455-543A-51

Query Match 7.2%; Score 190; DB 1; Length 2161;
 Best Local Similarity 18.5%; Pred. No. 1.8e-09;
 Matches 94; Conservative 83; Mismatches 155; Indels 176; Gaps 20;

QY 12 CRLGGWVPTGWRGLSLMGDVPVWSCRFCSSQDDGDRRLTYFQNLPESTLSL 71
 DB 333 CR--SGWVGPNCGI-----TFDNFAFAMLTIV 357
 QY 72 LVLLTANNPDVMIPIAYSKRAYA-----IFFTVTVIGSLFLMNLTAITYSQFGYLM 126
 DB 358 FOCITMEGTDLV---YWNDAIGWEMPVYFVSLIIGSFVLNLVGLSGEFSKERE 414
 QY 127 KSLQTSLFRRLGTAAFEVLSSWVG-----EGG-----APF----- 158
 DB 415 KAKARGDFQKLRKQOLEEDLKGIDWITQAEIDIPENEEGEGEGRKNTSMPTSETSV 474
 QY 159 -----QATRRGPSTSLRCPAPSSSATTTLTWTGSSPWOTWCF-----AC 201
 DB 475 NTENVSGEGENRCGCSL--CQAISSK-----LSRRMRMRNRRRCRAAVKSV 523
 QY 202 SMCWMOMCL-LSVMTSS-----WGF-----STASSLCTTQMSC-----CGRSLP--- 240
 DB 524 TTYMLVIVLFTLITISEHYNQDPWLQIODIANKVLLALFTCEMLYKMSLGLQAYF 583

```

0Y 241 -----NACBECTCPATCTGSSPLSCWBPENYGLSTLMDMTRLMLIVFEFR 230
DB 584 VSLFNRPCFPVCCGCTTETILVLEFIMSPG-----ISVRCVALLR 6255
0Y 291 IIPSKMAVVA5TVLGLVONMRAFGGILVVY--YFALITGINTLRCGYVALPGNSL 3473
DB 626 IEFVTRHMTSSNLVASLINSKMSIASLILLFLFIIFSLGMLGGRF-----676
0Y 348 APANASCCGSFEOLEYANNPFDEFAALVTLMMLAVYNNMO-VFLAIVRYSQPMK-- 404
DB 677 -----NDEFQTRSTFEDNFPOLLVTFQILTGEDMNAVMYDGIWAGPSSSGM 726
0Y 405 ---YFVLMMLVSSYIVWNLFLALILEM 429
DB 727 IVCITFIITLFCGNTIILNVLALAVDN 754

RESULT 5
US-08-223-305C-49
: Sequence 49, Application US/08223305C
: Patent No. 5851824
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: APPLICANT: Brenner, Robert
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/223,305C
: FILING DATE: April 4, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/866,354
: FILING DATE: April 10, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/116,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 52516 (P519739)
: TELECOMMUNICATION INFORMATION:

```

```

/ TELEPHONE: (619)238-0999
/ TELEFAX: (619)238-0062
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2161 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
US-08-223-305C-49

Query Match 7.2%; Score 190; DB 2; Length 2161;
Best Local Similarity 18.5%; Pred.No.1.8e-09;
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGWMPPTWVAVGLSLTLMGDPVYVWSCRFCSDDDGDGDRRLYYFOALPSPSLSL 71
DB 333 CR--SGWVGPNGI-----TDFDFAFAMLTIV 357
QY 72 IYLLFTANPDWMIAPYASKNRAYA-----IFFIVFVIGSLFNLMLIAIISOPRGYLM 126
DB 356 FCGITMEGTIVL---YMNNDLMGELPWPYIVSVLTIGSFYVNLVGLVLSGEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAPAEVLSSWVG-----EGG-----AFP----- 158
DB 415 KAKAGDFQKLEKQQLLEEDLKGVDWITQADIEDIPENEEGEGEKRTYSPMTSETESY 474
QY 159 -----QATRGPTSLSLFCRAPSSSSATTTLLTWGSSPWQTCPF-----AC 201
DB 475 NTEVSGEENGGCCGSL--COAISKSK-----LSRRRRRRNRNRRRCRAVKS 523
QY 202 SMCWMMQCL-LSVYITSS-----WGF--STASSLCTTCWSC-----CSRSLP--- 240
DB 524 FYYWLVIVLPLNTLTISEHYNQPDWLTQIDIANKVLALFTCEMLVKYMSLGDAQYF 583
QY 241 -----WAGBETCPPATCLTGSSPLSGWRPEWAGLSLMDTMLNMLYFRFLR 290
DB 584 VSLNRPDCFYVGGGITETITLIVLEIMSPLG-----ISVRCVRLLR 625
QY 291 IIPSKPAVVAASVTLGIVQNNRARGGLIVVY---YFAIIGINLFGVIALPGNSSL 347
DB 626 IEFVTRHMTSLSLNVLASLNSKMSIASLILLFLFTIIFSLDGMLPFGKPF----- 676
QY 348 APANGSAPCGSEQLLEYANNEDFPAALVTLMLNLMVNNMQ-VFLDAYRRYSGPWSK-- 404
DB 677 -----NDEDTQTRSTFDNFPQALLVFOILTGEDMNAVYDGMAYGGPSSSGM 726
QY 405 ---IYFVLMMVLSSVIVNLFALLEN 429
DB 727 IVCITFIIFLCIGNTILLNVLALAVDN 754

RESULT 6
US-08-223-305C-51
Sequence 51, Application US/08223305C
Patent No.5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA

```

```

ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-51

```

```

Query Match
Best Local Similarity 18.5%; Pred. No. 1.8e-09; Length 2161;
Matches 94; Conservative 83; Mismatches 155; Indels 176; Gaps 20;

```

```

QY 12 CRLLGGMWVPTGVNRGLLESLMGDVPVWVSCRFCSQDDGQDRRLTYFONLPESLSTL 71
DB 333 CR--SGWVGPNGI-----TINFNFAFMLTY 357
QY 72 LVLLTTANNPDVWIPAYSKNRAYA-----IFLIVFTVIGSLFLMNLTLTIYSQFQGYLM 126
DB 358 FOCITMEGWTVDL--YWNDAIGMEMVWYFVSLIILGSEFVLNLVGLVSGSEFKERE 414
QY 127 KSLQTSLEFRRRLGTRAFVLSMVG-----EGS-----APF----- 158
DB 415 KAKARGDFKLRKQOLEDLKGIDWITQADIDIPENEEGEGEGRKNTSMPTSETESV 474
QY 159 -----QATRGPSLTLFCRAPSSSSATTLTWTGSSPMQWCP-----AC 201
DB 475 NTENVSGBEENGCCSL--COALSKS-----LSRRRRRRWRFRNRRCRAVKSY 523
QY 202 SMCWQMCL-LSVMTS-----WGF--STASSLCTTCWSC-----CSRSLP--- 240
DB 524 TTYWLVIVLVFLNTLILISEHYNODPWLQIODIANKVLALLFTCEMLVKVYSIGQAYF 583
QY 241 -----WACEGTCPTATCIGSSPLSCMRPEMVGLLSLMDTRRLNMLIYRFLR 290

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DB 584 VSLFNRFDCEYVGGITETILELEIMSPLG-----ISVFRVRLR 625
QY 291 IIPSMKPMAYASTVLGLVONMRAFGILVYV---YFAIIGINLFRGIVALLPGNSL 347
DB 626 IFKVRHMTSLSLNVLASLNSMKSIASILLILFLFIIFSLIGMQLEGGK- 676
QY 348 APANGSAPCGSEFQOLEYMANNEDEFAALVTLMLVYNNMQ-VFLDAYRYSQPMK-- 404
DB 677 -----NFEDETQTKRSTFEDNFPQALLFVFOILGEDWNAVYDQIMAYGSPSSGM 726
QY 405 ---IFYVLMVLVSSVIVWNLFLALILEN 429
DB 727 IVCYIFILFLFCGNVYILLNVEFLATAYDN 754

```

```

RESULT 7
US-08-311-363-2
Sequence 2, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
City: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-2

```

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Query Match
Best Local Similarity 18.5%; Pred. No. 1.8e-09; Length 2161;
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

```

```

QY 12 CRLLGGMWVPTGVNRGLLESLMGDVPVWVSCRFCSQDDGQDRRLTYFONLPESLSTL 71
DB 333 CR--SGWVGPNGI-----TINFNFAFMLTY 357
QY 72 LVLLTTANNPDVWIPAYSKNRAYA-----IFLIVFTVIGSLFLMNLTLTIYSQFQGYLM 126
DB 358 FOCITMEGWTVDL--YWNDAIGMEMVWYFVSLIILGSEFVLNLVGLVSGSEFKERE 414

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; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1873 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-435-675B-4

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Query Match          7.1%; Score 186; DB 1; Length 1873;
Best Local Similarity 18.1%; Pred. No. 3.6e-09;
Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;

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QY 58 LTYFONLPESLSTLVLTLTANNDVMPAYSKNRAVA-----IEFIVTVGLSLFLML 112
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 272 ITHFDNFGFSLVYOCITHEGTDVL---YWNDAIGEMWPVYVTLTLLGSFELML 328
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 LTAIISQRYGLMKSLQSLFERRRLGTRAPEVLSSNVG----- 152
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 VLVGLSGEFTKEREKAKSGTFQKLEKQOLEEDLGRVSMWITQGVMDVEDLREGKLSL 388
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 -EGGAPQATR--RGPSTSLRFRASSSSATTLTWTGSSPWQTV---CPACS----- 202
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 389 EEEGSTESLEYELGINKITIQFR-----HWRQWNVFVWKCHDLVK 430
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 ---WCMQMC-----CLLSVMT-----SSWGSPSTAS 225
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 431 SRFYVLVILVALNTLSIASEHNQPLWTLHODIANVLLSLTIEMLKMTGLGRQ 490
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 226 SLCT-----TCMSCGRSLP--WACETCTPATCTLGSSPLSCWRPEVGLSLMDMTRM 279
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 491 YEMSIENRDCFYVCSGILLLVESGAMTP---LGISVLRC----- 529
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 280 LMLLYFRFLRIIPSKPAVAVATVGLYOMMRAFGGLIVVY---YVEATIGINLRG 336
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 530 -----IRLLRLFKITKYTSLSNLVASLINSIRSLASLLLEFLITIFALLGMQLFGG 583
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 VIVALPGNSSLAPANGSAPCGSFQOLEYVANNFDDFAALVTLMLNMYVNNM--QVFLDAY 395
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 584 RV-----DFEDTEVARSNFDFNPQALLSVFQVLIGEDMNSMTMYGI 624
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 396 RRYSGPWSK-----TYFVLMVLVSSVIVNLFALILENFLHMD-----KMDPSHL 440
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 MAYGGPSIVGVLCIYFIILVCGNYILLNVFLAIVNLAESLTSAKAKAEERRR 684
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 441 QPLAGTPEATYOMTEVLLFRDILPEPGEDELTERLSQHP 479
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 685 KMSRGLPKDT-----DEEKSVAKKLEQKP 709
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 10
US-07-745-206A-13
; Sequence 13, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann

```

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; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-13

```

```

Query Match          7.0%; Score 185.5; DB 1; Length 1754;
Best Local Similarity 24.6%; Pred. No. 3.7e-09;
Matches 83; Conservative 54; Mismatches 141; Indels 59; Gaps 13;

```

```

QY 149 SMVGGGAFPOAT-----RR-----GPSISLAFCR-APSSSATTTTLTWTG 188
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1082 ALDGPRESFVYVWTWKAKQGRRRMRKMGADGLSHRAPCSVAPPTCSASATTPG 1141
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 TSPWQTV-CPFACSWCMQMCCLLSVMT---SSWGFTASL---CTTCMSCGRSLPWA 242
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1142 TSRNFSMSSPAAPMLRQCAGTRGTINTYITSLVSLPRMSTWDCCGTLEP-- 1199
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 CEGTCPTPATCTLGSSPLSCWRPEMVGILLT---WDMTRMLNMLTYFRFLRIIPSKP 297
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1200 ISGTCGTFWTSIMSVAP--WWR-----LTSRKGKDINTIKSLRVLRLPLKTRLPK 1252
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 NAAVASVTLGLYOMMRAFGGLIVVYVPAIIGINLFRGVIALPGNSSLAPANGSAPCG 357
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1253 LKATFDCVANSKLAVLILYVLMFLMFTFAVIAVQLFKGFFYCTDESKLEDCRQYVL 1312
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 358 SFQOLEYWAN-----NEDDEFAALVTLMLNLMVNNMQVFL---DAYRRYSGPWS- 403
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1313 DYKEEVEAQPROMKKYDFHXDNVLMALLLFLFYSIGEGMPWLKKSVDATYEQGPSRG 1372
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 404 -----KIYFVLMVLVSSVIVNLFALILENFLHKWD 435
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1373 YRMELSTFYVYVYVFPFFFNIFVALIITTFQEOGD 1409
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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```

RESULT 11
US-08-311-363-13
; Sequence 13, Application US/08311363
; Patent No. 5876938
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert

```

TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-13

Query Match 7.0%; Score 185.5; DB 2; Length 1754;
Best Local Similarity 24.6%; Pred. No. 3.7e-09;
Matches 83; Conservative 54; Mismatches 141; Indels 59; Gaps 13;

QY 149 SMWGEGAFPOAT-----RR-----GPTSLRRCR-APSSSATTTLTWTG 188
DB 1082 ALLEGKPRSPFVVTWTKAKGRRRMRMTGAAPGLSSHTAPCSVAPPTCSASATTSFG 1141
QY 189 TSPWQW-CPPACSMCMQMCCLLSVMT--SSMGFSTASSL--CTTCWCCSRSLPWA 242
DB 1142 TSKRSEFMSWSPASPLLRQCOQTRGTLNLTWTFSLVSLRMRSTWDCFTLEP-- 1199
QY 243 CEGTCTPTATCLGSSPLSCWRBPMGLSL-----WDMTRMLNMLIVFFFLIITSMKP 297
DB 1200 ISGTGCFWTSLSVAP--WWR-----LBSRSKGDINTIKSLRVLRPLTKIRLPK 1252
QY 298 MAVVASVVLGVNQMRAPFGILVVVVYVFAIIGINLFRGVIALPGNSSIAPANGSAPCG 357
DB 1253 LKAIVEDCVNSLKNVILIVLMFMTFVIAVOLFKGFFCTDESKLEDCQYL 1312
QY 358 SFEOLEYMAN-----NEDDEAALVTLMNLMVNNMQLV---DAYRRYSGPWS- 403
DB 1313 DYKEEVEAQRQKWKDYDFHNDVLMALTLFTFVSTGECPMVLKHSVDATYEQGSFPG 1372
QY 404 -----KIYFVLMVLVSVIVNLFALILENFLHKWD 435
DB 1373 YRMEISIFVYVVFVFFEFVNIFFVALIITTFORQD 1409

RESULT 12
US-08-455-543A-45
Sequence 45, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0099
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1968 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-45

Query Match 6.8%; Score 178.5; DB 1; Length 1968;
Best Local Similarity 18.4%; Pred. No. 2.1e-08;
Matches 104; Conservative 80; Mismatches 175; Indels 205; Gaps 23;

QY 46 CSQDDGDRERLYFQNLPELSLTLVLTANNPDVIMIPYSKRRAVA-----IFFIV 100
DB 332 CKRWGNG-PKHGTINDNFAMFLVFQCITWEGTDLV---YVNDAGVGRDMPWIVYFT 387
QY 101 FTVIGSLFMTLITATITVQF-----RGYLMKSLQTSLE 134
DB 388 LIIGSFVILNVLGVLSGEFSKREKAKARGDFOLKREKQLEBDLGYLDWITQADBI 447

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QY 135 R-----RRIGTAAFEVLSMWGGAFAPOATR-----162
Db 448 XPENDEGMDKEERPNRGTGAG--MLDOKKGFAMFHSSTETHVSMPTSETESVNTENVA 505
QY 133 -----RGPSTSLRFGCAPSSSATTTTLTWTGTSPPWQWCPACSMC-----MMOM 208
Db 506 GGDIEGNCGARLAHRISKSK-----FSRYWRNRNRCRRKCRRAVKSVMFYMLVI 556
QY 209 -CCLLSVMT-----SSW-----GFSTASICT-----229
Db 557 FLVPLNTLTIASSEHYNQNMILEVODTANKALLALFTAEMLIKMYSLGLQAFVSLNRF 616
QY 230 TCMSCCSRLPWACGTCPTPATCITGSSPLSCWRPEVGLSLMDTMRMLNMLIVERFL 289
Db 617 DCFVVCGLIETI---LVEIKIMSPGLISVLR-----VRLRIFKXITRWNSL-----662
QY 290 RIIPSMKPMNAVASTVGLVONMRAFGIILVYV---YFAIIGINLFRGIYALPQNSS 346
Db 663 -----SNIVASLNSVRSIASLILLLFLFIITISLGMOLFGKF-----702
QY 347 LAPANGAPCGSPOLEYMANFDDFAALVTMLNMLVNNW--QVFLDAYRRYSGPWSK- 404
Db 703 -----NDEMOTRSTPFNFOQSLITVFQIITGEDMNSVMYDGI MAYGSPFP 751
QY 405 ----TYVLMWLVSSVIVMNLFLALILENF-----LHKWDPKSHLOPLAGT--PEA 449
Db 752 MLVCIFYFIIFISGNITLLNVLAIADNLADESLTSALKKEEERKRLARTASPER 811
QY 450 TYQMTVELLFRDILEEGEDELTE 473
Db 812 K-----QELVEKPAVESKE 826

RESULT 13
US-08-223-305C-45
; Sequence 45, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1968 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-45

Query Match 6.8%; Score 178.5; DB 2; Length 1968;
Best Local Similarity 18.4%; Pred. No.2,1e-08;
Matches 104; Conservative 80; Mismatches 175; Indels 205; Gaps 23;

QY 46 CSQDDGCDRELYTFQNLPESTLSLVLTTANNPDVIMPAYSKNRAYA-----IETIV 100
Db 332 CKPGWDG--PKHGTNDFNFAMLTVFQITWEGTDLV---YVNDVAGRDMPWLYEVT 387
QY 101 FTVIGSLFLMNLTLTIYSOF-----RGYLMKSIGTSLF 134
Db 388 LITISFVLNVLVGLVSGFSKEREKAKAGDFQKLEKQLEBDLGYIDMTIQADEI 447
QY 135 R-----RRIGTAAFEVLSMWGGAFAPOATR-----162
Db 448 XPENDEGMDKEERPNRGTGAG--MLDOKKGFAMFHSSTETHVSMPTSETESVNTENVA 505
QY 133 -----RGPSTSLRFGCAPSSSATTTTLTWTGTSPPWQWCPACSMC-----MMOM 208
Db 506 GGDIEGNCGARLAHRISKSK-----FSRYWRNRNRCRRKCRRAVKSVMFYMLVI 556
QY 209 -CCLLSVMT-----SSW-----GFSTASICT-----229
Db 557 FLVPLNTLTIASSEHYNQNMILEVODTANKALLALFTAEMLIKMYSLGLQAFVSLNRF 616
QY 230 TCMSCCSRLPWACGTCPTPATCITGSSPLSCWRPEVGLSLMDTMRMLNMLIVERFL 289
Db 617 DCFVVCGLIETI---LVEIKIMSPGLISVLR-----VRLRIFKXITRWNSL-----662
QY 290 RIIPSMKPMNAVASTVGLVONMRAFGIILVYV---YFAIIGINLFRGIYALPQNSS 346
Db 663 -----SNIVASLNSVRSIASLILLLFLFIITISLGMOLFGKF-----702
QY 347 LAPANGAPCGSPOLEYMANFDDFAALVTMLNMLVNNW--QVFLDAYRRYSGPWSK- 404
Db 703 -----NDEMOTRSTPFNFOQSLITVFQIITGEDMNSVMYDGI MAYGSPFP 751
QY 405 ----TYVLMWLVSSVIVMNLFLALILENF-----LHKWDPKSHLOPLAGT--PEA 449
Db 752 MLVCIFYFIIFISGNITLLNVLAIADNLADESLTSALKKEEERKRLARTASPER 811
QY 450 TYQMTVELLFRDILEEGEDELTE 473
Db 812 K-----QELVEKPAVESKE 826

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Search completed: October 8, 2002, 10:06:49
Job time : 31 secs

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-223-305C-48

Query Match 6.7%; Score 175.5; DB 2; Length 2237;
Best Local Similarity 19.6%; Pred. No. 5.1e-08;
Matches 105; Conservative 89; Mismatches 184; Indels 157; Gaps 24;

QY 36 DPVVPMS-----RFGSQDDGQDRE-----RLTYFQNLPELSLVLTTANPD 82
DB 261 EYVGDPPCKEAPARC--EGDTECREYWPGPFGITNFDNLFAILTVFCITMEGWD 318
QY 83 VMIPAYSKNRAYA-----IEFIYFVIGSLFLMNLTLTAIYSQF-----RGYLMK 127
DB 319 IL---YNTNDAGNTWMNLIYFIPLIIGSFELNLVGLVGEFAKERERVENRRAPLKL 375
QY 128 SIQTSLEFRRRLG-TRAAFEVLSWVGEAGAPPQATRRGPSTSLRCPAPSSSATTTLT 186
DB 376 RROQOIERLNGYLEMIFKAEEVMLAEEDR--NAEKSPLDYLK--RAATKKSNDLIHA 431
QY 187 WGTSSPMQWTWC---PF-----ACSWCMQMC- 209
DB 432 EGEGERPADLCAVGSPPFARASIKSGKTESSTYERRKEMFRFFIRMWKAOSFYWVYLCV 491
QY 210 -CLLSVMTSSWGFSTASSICTTCWSCCSRSIPWACEGTCPTATC-LTGSSPISQWPE- 266
DB 492 VALNTLCVAMVHYNQPRRLTTLTYFA-----EFVFLGLFLEMSIKMTGLGPRSYFRSSF 546
QY 267 -----WVGLL--SLMDTKM-----LNMILVRFELRIIPSMKPMAYVASTVLGLVQNM 312
DB 547 NCFDEGVAVGSVEYVMAIKPGSSFGISVLRALRLRIEFKVTYWSLSRLNLYVSLNSM 606
QY 313 RAFGSILVVV---YFAIIGINLFRGYIVALPGNSSLAPANGSAPGSEFQLEFYMANNF 369
DB 607 KSIISLFLFLFLFIVFALLGMOLFQGF-----NFQD-ETPTTNF 646
QY 370 DDEFAALVTLNMLNMYNNQVFLDAYRRY-----SGPMKRYFVLMWLVSSYIWNLF 422
DB 647 DTFPAALITVFOILTGEDMNAVM--YHGIESQGVSKGMFSSFYFIVLTLEGNVTLNLF 704
QY 423 LALILENFLHKWDRSHQPLAGTPEATYQNTVLLERDILEEPGEDELTERLSQ 477
DB 705 LAIAYDN-----LANAOELT-----KDEEMEAANO 731

•
•
•

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:56:21 ; Search time 42 Seconds
(without alignments)
1109.603 Million cell updates/sec

Title: US-09-918-359-7
Perfect score: 2634
Sequence: 1 MSSACWEGATGRCRLGGGMV.....PGEDELTERLSQHPHMLCR 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1180	44.8	371	T46421	hypothetical prote
2	345	13.1	819	JC7240	two-pore calcium c
3	342	13.0	724	B65045	probable calcium c
4	197	7.5	2181	A38198	calcium channel al
5	194	7.4	2222	A37490	voltage-dependent
6	194	7.4	2272	C54972	voltage-dependent
7	190	7.2	1610	A46227	voltage-dependent
8	190	7.2	2161	JH0564	calcium channel al
9	189.5	7.2	2223	A47447	calcium channel pr
10	189.5	7.2	2262	T30890	calcium channel al
11	189	7.2	2270	A54972	voltage-dependent
12	187	7.1	2178	S29237	calcium channel pr
13	187	7.1	2259	S29236	calcium channel pr
14	186.5	7.1	2251	B54972	voltage-dependent
15	186	7.1	1873	A30063	dihydropyridine re
16	185	7.0	1646	JH0422	voltage-dependent
17	184	7.0	2220	A45290	calcium channel pr
18	180	6.8	2166	S11339	calcium channel al
19	179.5	6.8	2171	S05054	calcium channel al
20	178.5	6.8	2203	T42742	voltage-dependent
21	177	6.7	2139	A44467	voltage-dependent
22	176	6.7	1873	A5645	calcium channel, v
23	175.5	6.7	2237	T45115	N-type calcium cha
24	175.5	6.7	2339	A42566	omega-conotoxin-se
25	171	6.5	2254	T09053	low voltage-activa
26	168	6.4	2336	A45386	omega-conotoxin-se
27	167	6.3	1657	T15838	hypothetical prote
28	165.5	6.3	2143	JH0427	voltage-dependent
29	164.5	6.2	2273	I46477	calcium channel BI

30	164.5	6.2	2424	2	I46480	calcium channel BI
31	163.5	6.2	1687	2	S41742	calcium channel al
32	163	6.2	1852	2	A37860	calcium channel pr
33	161	6.1	1739	2	A48298	sodium channel hom
34	160.5	6.1	2108	2	S72458	sodium channel pro
35	160.5	6.1	2212	2	A41098	calcium channel pr
36	160	6.1	1559	2	T30535	calcium channel al
37	159.5	6.1	2019	2	A33996	sodium channel pro
38	159	6.0	274	2	E83837	hypothetical prote
39	159	6.0	1951	2	S00320	sodium channel pro
40	159	6.0	1983	2	A60054	sodium channel pro
41	158.5	6.0	1784	2	T43167	sodium channel pro
42	158.5	6.0	1810	2	T31092	probable voltage-g
43	158	6.0	1783	2	T37258	probable voltage-g
44	158	6.0	1917	2	C88728	protein C48A7.1 [i
45	156.5	5.9	2288	2	S41080	calcium channel al

ALIGNMENTS

RESULT 1

T46421
hypothetical protein DKFZp434M0223.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46421

R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A:Reference number: 223034

A:Accession: T46421

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-371 <AAA>

A:Cross-references: EMBL:AL137479

A:Experimental source: adult testis; clone DKFZp434M0223

C:Genetics:

A>Note: DKFZp434M0223.1

Query Match

Best Local Similarity 44.8%; Score 1180; DB 2; Length 371;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	263	WRPEWGLSLDMTRMLNMLIVFRLRTIPMKPAAVAVSVGLGVOMRAFGILVYV	322
DB	149	WRPEWGLSLDMTRMLNMLIVFRLRTIPMKPAAVAVSVGLGVOMRAFGILVYV	208
OY	323	YVFAIIGINLFRGVIVALLPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAALVTLMNL	382
DB	209	YVFAIIGINLFRGVIVALLPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAALVTLMNL	268
OY	383	MYVNNWQVFLDLYRRYSRGSWSKIYFVLMVSVSVIVNLFLLILENPLHKKDPSSHOP	442
DB	269	MYVNNWQVFLDLYRRYSRGSWSKIYFVLMVSVSVIVNLFLLILENPLHKKDPSSHOP	328
OY	443	IAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHPHMLCR	485
DB	329	IAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHPHMLCR	371

RESULT 2

JC7240
two-pore calcium channel protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C:Accession: JC7240

R:ishibashi, K.; Suzuki, M.; Imai, M.

Biochem. Biophys. Res. Commun. 270, 370-376, 2000

A:Title: Molecular cloning of a novel form (two-repeat) protein related to voltage-ga

A:Reference number: JC7240

A:Accession: JC7240

A:Molecule type: mRNA

A:Residues: 1-819 <ISH>

A:Cross-references: DBJ:AB018253
A:Experimental source: kidney
C:Comment: This protein is a phosphorylated transmembrane glycoprotein having characteri
C:Keywords: glycoprotein; kidney; transmembrane protein

Query Match 13.1%; Score 345; DB 2; Length 819;
Best Local Similarity 25.7%; Pred. No. 7e-20;
Matches 117; Conservative 71; Mismatches 164; Indels 104; Gaps 18;

QY 60 YFNPESLTSLLVLTANNPDVMIIPAYSKNRAVAIFIVFYVIGSLFIMNLTAIYS 119
DB 263 YFNTLSINYLVTLLTAFTFPMPSYRNWSCVFETVYLTIELYIMLLAVFD 322
QY 120 QFNGYLMKSLQTSFRRRLGTRAAFEVLSMVEGSAF-----POATRRGPST 167
DB 323 TFDIDIEKHKFKSLLLKRAIOHAHILYQRRPAGISTYQFEGMLAFYPRASAR 379
QY 168 SLRFCAAPSSSSATTTLT-----WGTSPPQWV---CPFACSCMCMQCC 210
DB 380 --RFLTFKALNQSTPLSLKDFYDIYVAALQMKAKKNQHWDELPRATFLFKG 434
QY 211 LLSVMTSMGFSASSLCT---CW-----SCCRSLPMACEGCPATPACLT 255
DB 435 --TILVNSKAFQYFMTLVAVANGVWILVETEMKGGFISKHVPWST-----LVFLTI 486
QY 256 -----GSSPL-----SCWRP-----EMVGLSLMDMTRLNM-----LIVFR 287
DB 487 YGVELFMKAVAGLDPVEYELSSGMNLPDESLLAFALFGLAL-----TLNMPFYVILRP 541
QY 288 --FLRIIPSKPAVAVASTYVLGVONKRAFGILVVYVYFAITIGLNGVT---VALP 342
DB 542 LQLRFEKTKKRRYVLDTFEELLPRMASLGLTLTFEYVFAIVGMFFSGRLSPNCSTP 601
QY 343 GNSSLAPANGS-APCGSEQL-----EYMANNDFAAIVTLNLMVYNNWQVFLAYR 397
DB 602 ARRGFLPIDSTRIGKTKFGKGYIYLNPNILNSFTLFEVYVNNWYIMESVTS 661
QY 398 YSGPMSKIYFVLMVSVIWNLFALILENFLHK 433
DB 662 QTSWRSRLYFMTFYITMV-MTIIVAFLEAVFR 696

RESULT 3

B85045
probable calcium channel [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: B85045
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: B85045
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-724 <STO>
A:Cross-references: GB:NC_001268; NID:g7270679; PIDN:CAB7841.1; GSPDB:GN00140
C:Genetics:
A:gene: AT4G03560
A:Map position: 4

Query Match 13.0%; Score 342; DB 2; Length 724;
Best Local Similarity 24.1%; Pred. No. 1.1e-19;
Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;

QY 55 RERLYFQNLPESLTSLVLTANNPDVMIIPAYSKNRAVAIFIVFYVIGSLFIMNL 114
DB 233 QOGLTFVTSYGATLYOMFIETTSNNDPMIPAYKSSRMSSVFVLYLVIGVFNLL 292
QY 115 AIITYSFRGILKMSIQ-TSLFRRRLGTRA-----AEVYSS----- 149
DB 293 AAVYDSFKQLAKOVSGDMQKRRMLEKAFGLIDSKNGEIDKNOCIKILEQTLNRYTLP 352

QY 150 --WVEGGA-----PPQATRRGPST 167
DB 353 KISKEEGLTFDELDDTRDKINKDEFADLCQALRFOKEVPSLEHNPQIYHSLSQ 412
QY 168 SLR-FCRAPSSSA-----TTTLTTWTSS--PMQWCPFACSCMW-MQMC 209
DB 413 QLRAPSPNFGVAISPLIINFIAVVEFTLLDEESSAQPMQV-AEFVGMIVYLEMA 471
QY 210 CLLSVMT-----SSW--GFSSSLCTTCWSCCSRLPMACEGCPATPACLTGSSPLSCW 263
DB 472 --LKIITYGFEWNRREGANFDELVT-----VVI-VIGTATFIT----- 508
QY 264 RPEVGLSLMDMTRLNMLIVFRFLRIIPSKPMAVAVASTYVLGVONKRAFGILVVY 323
DB 509 -PENTFFSGEMIRYLLARMLRILFLMNVQRYRAFITFTLIPSLMPTIGTICVL 567
QY 324 YVFAIGINLFRGYVALPONSLSLAPANGSAPCGSEF---QLEYMANNDFAALVTL 379
DB 568 CIYCISIGVQVFGGLVNA--GNKKL-----FETELAEDDYLLFNNDYPNGKVT 614
QY 380 WNLVYNNWQVFLDAYRYSGPSKI-YFVLMVSVIWNLFALILENFLHKMD 435
DB 615 FNLLVGMNQMVMESTKDLGTWMTSTYFVYITILLNLVAVFLAEAFTELD 671

RESULT 4

A38198
calcium channel alpha-1 chain, pancreatic - human
N:Alternate names: Delta cell-type calcium channel alpha-1 chain; neuroendocrine-type
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A38198
R:Seino, S.; Chen, L.; Seino, M.; Blondel, O.; Takeda, J.; Johnson, J.H.; Bell, G.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 584-588, 1992
A:Title: Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expres
A:Reference number: A38198; MUID:92115705
A:Accession: A38198
A:Molecule type: mRNA
A:Residues: 1-2181 <SEI>
A:Cross-references: GB:M83666; NID:g179751; PIDN:AAA5629.1; PID:g179752
A:Experimental source: pancreatic beta cells
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: membrane protein; voltage-gated ion channel

Query Match 7.5%; Score 197; DB 2; Length 2181;
Best Local Similarity 18.2%; Pred. No. 1.7e-07;
Matches 93; Conservative 81; Mismatches 175; Indels 162; Gaps 17;

QY 12 CRLGGMMVPTGWRGLSLMGDDPVWMSCRCSQDDGODRRLTYFQNLPESLTSL 71
DB 333 CR--SGWVGNNGI-----TNDNFAMFLVY 357
QY 72 LVLLTANNPDVMIIPAYSKNRAVA-----IFIVFYVIGSLFIMNLTAIYSGFRGYLM 126
DB 358 FOCITMEGWTDLV--YVWDAAGWEMPVYFVSLIIGSFVNLNLVGLSEF----- 409
QY 127 KSLQTSFRRRLGTRAAFEVYSS-----WVEGGAFPQATRRGPSTSLRFC 172
DB 410 -----SKEREKAKARGDFQLRKQOLEEDLKGILDMITQAEIDIDPENEEGEGEGRNT 464
QY 173 RAPSSSATTTTLTTWTSSPMQWCPFACSCMCMQCLLSVMTSS--WGFSSSLCT 229
DB 465 SWPTSE--TESVMTENVSGEENRGCGSLMCMWRRAKAGAPSGGRMRGQAISSKLS 522
QY 230 TCWSSCSRLPMACEGICPPA-----TCLTGSSP----- 259
DB 523 RRRRRNNRRRRRCRAAVKSVTFYVLYLVFLNTLTLSSEHYNODPWLQIODIANKYL 582
QY 260 LSCWREP-----VGLSLMDM-----TRMLNMLIV-----FR 287
DB 583 LALFTCBMLVKMTSLGLQAVFVSLFNRPDFVVCGITTEITIVELTMSPLGISVRCVR 642

```

QY 288 FLRIIPSMKPAVAAYATVLGVOMAKRFGILVYV---YFALIGINLFRGYVALPGN 344
D6 643 LLRIFFKTYRHTTSSNIVASLINSMKSIASLILLLFFIIIFSLIGMQLFGRF----- 696
QY 345 SSIAPANGSAPGSGFEOLEVANNFDEPAALVTLMLMLVNNMQ--FELDAYRYSQPS 403
D6 697 -----NFDETQTKRSFEDNFPOALLVTFQILTGEDMNAVMYDGI MAYGPPS 743
QY 404 K-----IYFVLMVLVSSYIVWNLFLATILLEN 429
D6 744 SGMIVCYIFILLFCNGNITLNNFLATAVDN 774

```

RESULT 5
A37490
voltage-dependent calcium channel alpha 1E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A37490
R:Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A:Title: Structure and functional expression of a member of the low voltage-activated calcium channel family
A:Accession: A37490; MUID: 93262464

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2222 <S00>
A:Cross-references: GB:IL15453; NID:g310082; PIDN:AAA0855.1; PID:g31008
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:13101)
A:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match	7.4%	Score 194;	DB 2;	Length 2222;
Best Local Similarity	20.8%	Pred. No. 3e-07;		
Matches 113, Conservative	86;	Mismatches 221;	Indels 122;	Gaps 21

QY 32 LMGSGPVVWWSCREFSQQDDGOD---RERLTFYQNLPBESTSLVLTTTANNPDVWIPA 87
| | | : : : : :
Db 210 LEFDFDPHPCGVGGCPAGYECKDWIGPNDGTGFQDNILEAVLTIFYQCITMGCWTYYL--- 266

QY 88 YSNRRAYA----IFFIVFVIGSLFMNLTPIIYSQE-----RCYLKMSLQTS 132
| : |
| : || :|| :|| : : : |
Db 267 YNNNDALGATWNWLYEIPLIIGSEFLNLTVCVLGSGEAKEREVEYNRRAFMKLRQQO 326

```

QY 133 LERRRLGTRA---AFEVL--SSMVGEGAFQATRRGPSTSLR--FCRAPSSSSATITLL 184
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 IERELNGYAWIDKAEVMALEFNKNGSTALEVLRRAATIKRSRTREAMTRDSDDEHCVDI 386

```

Oy 185 TWWGT----SSPWQWCPFACSWCMQMCCLLSY--WTSS----WGFTASLCTTCWSC 234
 ::::| | | | | : | | | | | : | | | |
Db 387 SSVGTPLARASTKTKVDGASYFRHKERLLRISIRHWAKSQVEFWIVLSVALNTACVAI 446

```

QY      235 CSKSLP-WACE-----GTCPPATCLGSSPLSCMR-PEMYGL 270
      : | | | | | | | | | | | | | | | | | | | | |
Db      447 VHHNQPMQTHLLTYAAEFLPLGLFLEMSLKMYGMGR---LYFHSSFNCFDEGTVVGS 502

```

Qy 271 L---SLMDMTRM-----LNMILVFRFLRIIPSMKPMAYASTVLGLYQNMRAGFGLVVY 323
:
: : : | : : : | : : : | : : : | : : :
Dd 503 IFEVVMATFRPGTSGISVLRALRLRIRFKITKYMASLNLYVLSMSMKSIISLEFLF 5622

QY	324	---YFAIGINLFRGVIVALPGNSSLAPANGSAPCGSEQLKXANNEDDFAALVTLM	380
		:::	
Db	563	LEIVFALLGMQLFGGRFNNDGTBSA-----NFTFEPAAIMTVF	602

QY 381 NLMVNNM-QVFUDAYRRY---SGPMSKIYFVLWMLVSSVINWLEFLALLENFL----- 431
:: :| :| :| - | | | | | : : :| :| :| :|

Dd 603 QLTGEDNNEVMYNGIRSGGVSSCGMMSAIFYLTLTGNYTLINVELAIVDNLNAOE 662

```

QY 432 -----HKWDRSHQLAGTPEATYQMTVELFRDILEBCEDEITERLS 476
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 LTKDEEEEFNOKHALQAKESVSMAPNPNSTIERRRRRHHMSMWERRSSHLERR 722

```

QY 477 QH 478

Db 723 RH 724

RESULT 6
C54972

Voltage-dependent calcium channel alpha 1E - mouse
C.Species: Mus musculus (house mouse)
C.Date: 12-Apr-1995 #sequence-revision 12-Apr-1995 #text-change 24-Sep-1999
C.Accession: C54972
R.Williams, M.E., Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;
J. Biol. Chem. 269, 22344-22357, 1994
A.Title: Structure and functional characterization of neuronal alpha-1E calcium channel
R.Reference number: A54972; MUID:94350992

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Residue type: mRNA
A:Residues: 1-2272 <MIL>
A:Cross-references: GB:129346; NID:g5522330; PIDN:AAA59206.1; PID:g5522331
A:Note: authors translated the codon AGG for residue 788 as lysa, and Cct for residue
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match	7.4%;	Score 194;	DB 2;	Length 2272;
Best Local Similarity	20.8%;	Pred. No. 3.1e-07;		
Matches 113;	Conservative 86;	Mismatches 221;	Indels 122;	Gaps 21;

QY 32 LMGDPVAVWMSCRFCSQQDDGOD---RRLTYQLNPESLSTSLVLTTANPNPDMIPA 87
| | | : : : : :
Db 260 LEGFDPPHPCGVGGCPAGYECKDWIGPDNGITQGFNDILEAVLTVPQCITMCGWTIVL--- 316

QY 88 YSKNRAYA-----IFFIVFVIGSLFMNLTAIYSOF-----RCYLMSKIQTS 132
| : | ::|| ::|| :|| : : :| | : :
Db 317 YNNNDALGATWNNLXEIFPLIIISFEVLNLTGVLSGEAKEREVENRRAFMKLRQQQ 376

```
QY 133 LRRRLGTRA---AFEVL--SSMGEAGAPDTRCPSTSLR--FCRAPSSSSATYTL 184
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 377 IEEELNGYAWIDKAEVLMLEENKNSGTSALEYLRRAIKRSREAMTDDSSDEHCVDI 436
```

QY 185 TWGCT-----SSPWQTWCPFCASWCMMQMCCLLSY--MTSS---WGFSSTASSICTTCWSC 234
:::| | | | : | : | : | : | : | : | : | :
Db 437 SSVGTPLARASIKSKVDGASYFRHKERLLRISIRHMYSQVFYIVLSTVALNTACVAI 496

```

OY      235 CCRSLP-WACE-----GTCPTPATCLNGSSPLSCWR-PEMAYGL 270
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      497 VHNQPOWHTLTLTYAEFLPLGLFLEMSLKMYGMGR---LYHSSNCFDFCYVGS 552

```

```
QY      271 L--SLMDNTRM-----LNMLVFRFLRIIPSMKPMAYASTVLGLVNRAFGILVVY   323
       :  :: |  |||  |  |  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
Db      553 IFEVVMALFRPGISFGISVLRALRLIRIFKTIKYWASLNLNVLSMSKSIIISLFLEF   612
```

```

QY      324 ---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSEQLKXWANNEDDFAALVTLM 380
          |||::: || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      613 LFIIVEFALIGMQLFGGRFNNDGTBSA-----NDFEPAALMTVF 652

```

```
QY      381 NLMVVNNM-QVFLDAYRRY---SGDWSKIYFVLWLVSSIVINVLFLAILLENFL---- 431
       :: : : : : | | | | | : : : : : : :
Db      653 QLTGDMNEVMYNGIRSGCGSSGMMSAITFYLTTFGNYYTLINVFLLAIADVNTANAOE 712
```

```

QY      432 -----HKWDBRSHLQPLAGTPEATYQMTVELFRDILEEGEDELTERLS 476
          |      :  |  :  :      :  |  :  |
Db      713 LTKDEQEEEFNOKHALQAKESVSMAPNPSIERRRRRHHHMSMWEPSSHLERRR 772

```

QY	477	QH	478
	:		
Db	773	RH	774

RESULT 7
A46227

C:\Species: Mesocricetus auratus (golden hamster) #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:\Date: 27-Oct-1993
C:\Accession: A46227

R;Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.;
Mol. Endocrinol. 6, 2143-2152, 1992
A;Title: Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel fro
A;Reference number: A46227; M01D:93149124
A;Accession: A46227
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1610 <YAN>

A;Experimental source: Insulin-secreting cell line HIT-T15
A;Note: sequence extracted from NCBI backbone (NCBI:P123692)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 7.2%; Score 190; DB 2; Length 1610;
Best Local Similarity 17.9%; Pred. No. 4.5e-07;
Matches 91; Conservative 86; Mismatches 174; Indels 158; Gaps 18;

QY 6 WEATGR-CRLGG-----GMVPPGVRGLSLMGDDPVVWSCRCSQDDGDRRLT 59
DB 318 FSGNGRCVAVGTECRSGVWPNNGI-----T 344
QY 60 YFQNLPSLTLVLTANNPDVMPAYSKNRVA-----IFPIVTVIGSLFIMNLIT 114
DB 345 NEDNFAFAMLVFOCITMEGTVDL---YMNDAFGELFWVTVFVSLVIGSFVNLVL 401
QY 115 AIISQFRGYLMSLQTSFRRRLGTRAFEVLSMWG-----EGAFPPQA 160
DB 402 GVLSEGEKREKAKARGDQKLENEQLEDLKGVLDTTQADIDPENEEBEGEGKR 461
QY 161 TRRQPSLSLRCAAPSSSATITLTWGT-----SSPWQWCPF-----A 200
DB 462 NTSMTSETESVNTENYSGEGTQSGSLQALSKSLRRMRNRNRNRRAVKS 521
QY 201 CSWCMQMCCL-LSVMTSS-----WGF-----STASSLCTTQWSC-----CSRSLP-- 240
DB 522 VTFWLVIVLVFNTLTISSEHYNPQDMLQIODINKVLLAFTCEMLYKMTSLGIQAY 561
QY 241 -----WACEGTCPPATCLTGSSPLSCWRPENVGLSLMDTRMLNMLYFRFL 289
DB 562 FVSLFNRFDCFVCGGITETILVELLMSPLG-----VSFRCVRL 623
QY 290 RIISMKPMVAVSTVGLVONMRAFGILVYV---YVFAIGINLFRGVIALPQNS 346
DB 624 RIFVTRHMTSLSLNVLASLNSKMSIASLLLEFLFIIFSLGMOLFGEKF----- 675
QY 347 LAPANGSAPCGSFQLEWANNEDFAALVTLMNLVNNWQ-VFLDAVRRYSGPMSK- 404
DB 676 -----NFDETQKRTSTFDFNFPQALLTVFOILTGEDMNAVMYDGMAYGPPSSSG 724
QY 405 ---IYFVLMVLVSSVIVNLFALILEN 429
DB 725 MIVCIYFIILFCIGNYILLNVLAIADN 753

RESULT 8

JH0564
calcium channel alpha-1D chain - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Nov-1999
C;Accession: JH0564
R;Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellistebl, G.; Ellis, S.B.;
Neuron 8, 71-84, 1992
A;Title: Structure and functional expression of alpha1, alpha2, and beta subunits of a
A;Reference number: JH0564; M01D:92110010
A;Accession: JH0564
A;Molecule type: mRNA
A;Residues: 1-2161 <WIL>
A;Cross-references: GB:M76558
A;Experimental source: neuroblastoma, cell line IMR32
C;Comment: This protein is a subunit of the voltage-dependent calcium channel.
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein
F;127-145/Domain: transmembrane #status predicted <IS1>
F;164-183/Domain: transmembrane #status predicted <IS2>

F;195-214/Domain: transmembrane #status predicted <IS3>
F;236-254/Domain: transmembrane #status predicted <IS4>
F;274-293/Domain: transmembrane #status predicted <IS5>
F;382-406/Domain: transmembrane #status predicted <IS6>
F;524-542/Domain: transmembrane #status predicted <IS7>
F;558-577/Domain: transmembrane #status predicted <IS8>
F;586-603/Domain: transmembrane #status predicted <IS9>
F;615-633/Domain: transmembrane #status predicted <IS10>
F;653-672/Domain: transmembrane #status predicted <IS11>
F;728-752/Domain: transmembrane #status predicted <IS12>
F;888-905/Domain: transmembrane #status predicted <IS13>
F;922-941/Domain: transmembrane #status predicted <IS14>
F;954-972/Domain: transmembrane #status predicted <IS15>
F;980-998/Domain: transmembrane #status predicted <IS16>
F;1018-1037/Domain: transmembrane #status predicted <IS17>
F;1128-1152/Domain: transmembrane #status predicted <IS18>
F;1206-1224/Domain: transmembrane #status predicted <IS19>
F;1240-1259/Domain: transmembrane #status predicted <IS20>
F;1268-1286/Domain: transmembrane #status predicted <IS21>
F;1315-1333/Domain: transmembrane #status predicted <IS22>
F;1353-1372/Domain: transmembrane #status predicted <IS23>
F;1440-1464/Domain: transmembrane #status predicted <IS24>

Query Match 7.2%; Score 190; DB 2; Length 2161;
Best Local Similarity 18.5%; Pred. No. 6.1e-07;
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGWVPTGVNGLSLMGDDPVVWSCRCSQDDGDRRLTYFQNLPSLTL 71
DB 333 CR--SGWCPNNGI-----INFDFAFAMLV 357
QY 72 LVLTANNPDVMPAYSKNRVA-----IFPIVTVIGSLFIMNLTAIISQFRGYL 126
DB 358 FQGITMEGTVDL---YMNDAFGELFWVTVFVSLVIGSFVNLVLGVLSEGEKRE 414
QY 127 KSLQTSFRRRLGTRAFEVLSMWG-----EG-----AFP----- 158
DB 415 KAKARGDFKRLKQLEDLKGVLDTTQADIDPENEEBEGEGKRNTPSETESV 474
QY 159 -----QATRRQPSLSLRCAAPSSSATITLTWGTSSPWQWCPF-----AC 201
DB 475 NTENYSGEGENKCCGSL--CQALSKS-----LSRRRRNRNRNRRAVKS 523
QY 202 SWCMQMCCL-LSVMTSS-----WGF-----STASSLCTTQWSC-----CSRSLP-- 240
DB 524 TFWLVIVLVFNTLTISSEHYNPQDMLQIODINKVLLAFTCEMLYKMTSLGIQAY 583
QY 241 -----WACEGTCPPATCLTGSSPLSCWRPENVGLSLMDTRMLNMLYFRFL 290
DB 584 VSLFNRFDCFVCGGITETILVELLMSPLG-----ISVRCVRL 625
QY 291 RIISMKPMVAVSTVGLVONMRAFGILVYV---YVFAIGINLFRGVIALPQNS 347
DB 626 IEFVTRHMTSLSLNVLASLNSKMSIASLLLEFLFIIFSLGMOLFGEKF----- 676
QY 348 APANGSAPCGSFQLEWANNEDFAALVTLMNLVNNWQ-VFLDAVRRYSGPMSK-- 404
DB 677 -----NFDETQKRTSTFDFNFPQALLTVFOILTGEDMNAVMYDGMAYGPPSSSG 726
QY 405 ---IYFVLMVLVSSVIVNLFALILEN 429
DB 727 IYCIYFIILFCIGNYILLNVLAIADN 754

RESULT 9

A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommat
C;Species: Discopyge ommat
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A47447
R;Horne, W.A.; Ellinor, P.T.; Iman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray D

A:Reference number: A47447; MUID:93248175

A:Accession: A47447

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2223 <HOK>

A:Note: sequence extracted from NCBI backbone (NCBI:130671)

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 7.2%; Score 189.5; DB 2; Length 2223;

Best Local Similarity 19.9%; Pred. No. 6.9e-07;

Matches 107; Conservative 87; Mismatches 197; Indels 147; Gaps 25;

```

QY 43 CRRCSQDDGDRRLTYFQNLPESTLSLVLTTANNPDVWIPAKSKRAVA-----IF 97
Db 291 CSYWGPNMG-----ITQFDNIFALLTFVQCITMEGWTTL--YNDLALGAMWNVY 342
QY 98 FIVFTVIGSLFLMNLTLTAIYSQF-----RGYLMKSLQTSLEFRRIGTRA---A 143
Db 343 FIPLIIGSFYVNLVGLVLSGEFAKERERVENRRSFELRRQOIERELNGYRAMIDKA 402
QY 144 FEVL-----SSMVBEGGAFPOATRNG--PSTSLRRCRAPSSSATTTLTWTGTSNP 192
Db 403 EEVMLEENKNAGEKSA--HYLRATIKKGRREMIQTSSSDQYTEISSV--SPLARAS 459
QY 193 -----W-----QTWCPFACSW---CMQ 207
Db 460 IKSTKLEGGSSYFRKKEMLRISIRHWKSHAFYIVLGLVALNTVCVAVVHYDQPLMLS 519
QY 208 MCCLISVMTSGWSEFSTASLCTTCWSCCRSLPWACKEGTCPTPATCLGSSPLSCMR--PE 266
Db 520 NEFLYAETFLGLFS--SEMFLLKMYGGGPR-----LYHSSFECEGCGV 561
QY 267 MVGLL--SLMDTRM-----LNLIVFRFLIIPSKPMAVAVSTVLGLVONKRAFGIL 319
Db 562 IIGSIFDVWTTIIPETPSFGISVLRALRLRIEFTIKYMASLRNLVYLSMSKSIISL 621
QY 320 VVVT--YVFAIIGINLFRGYVALPGNSSILAPANGSAPGSEFQLEVMANNDDPAAL 376
Db 622 FLLEFLVFFVALLCMQLEFG-----QNFEEGTRP-----TNDFTPPAAI 661
QY 377 VTLNMLVAVNM--QVFLDAVRRY---SGPWSKIYFVLMVLSVIVNLFALLILENFL 431
Db 662 ITVFQIILTGDDWMEVYNGIKSGGVGMSWVYFVTLTFNGNYTLNFAIVADNLA 721
QY 432 HKMDPRSHLOPLAGTPRATYQMTVELFRDI--LEEGDEELTERISQPH--LMLCR 485
Db 722 NAQELTKEDQ---EEBAIQKHALOKAKAEVSPASGPEPSTEREFRHRHMSWEAR 776

```

RESULT 10

T30890

calcium channel alpha1-chain - sea squirt (Halocynthia roretzi)

N:Alternate names: ascidian calcium channel alpha1-subunit

C:Species: Halocynthia roretzi

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000

C:Accession: T30890

R:Okamura, Y.; Okagaki, R.

submitted to the EMBL data library, May 1998

A:Description: TUCAL, ascidian calcium channel alpha1-subunit.

A:Reference number: 220924

A:Accession: T30890

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2262 <OKA>

A:Cross-references: EMBL:AB013604; PIDN:BA434927.1

A:Experimental source: young tadpole larvae

C:Genetics:

A:Gene: TUCAL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: calcium binding; calcium channel

Query Match 7.2%; Score 189.5; DB 2; Length 2262;

Best Local Similarity 20.2%; Pred. No. 7e-07;

Matches 99; Conservative 76; Mismatches 159; Indels 157; Gaps 20;

```

QY 33 WGGDVPVWMSRFGS-----QDDGDRRLTYFQNLPESTLSLVLTTANNPDVWIPA 87
Db 371 WG-----RCSGNGICESDWAGSPKGIINDTFYFAVITVQCITMEGWTDLV--- 418
QY 88 YSKNRAYA-----IFFIVFTVIGSLFLMNLTLTAIYSQFGRYLMKSLQTSLEFRRIGTRA 142
Db 419 YNMDAVGNLMPLWYIFSLIIGSFYVNLVGLVLSGEF-----SKERKANARG 468
QY 143 AFEVL-----SSMVBEGGAFPOATRNGP-----STSLRRCRAPSSSATTTL 184
Db 469 EFQRLRKOQTDMDKGYMDMTITQAEIDLDPNEDREDRRSASNEQDNDADSEVSGIQID 528
QY 185 TTWGT-----SSPQWT-----CPF-----ACSNQWQW-----CCLISVMTSSW 219
Db 529 ETWQMQRRALFKYCYRRRRRRNRKTRRCRKYVSKSPYVLYLVFCNTLSLATEHY 588
QY 220 GFSTASLCTTCWSCCRSLPWACKEGTCPTPATCLGSSPLSCMRPEM----- 267
Db 589 -----RQPPWL-----TLQDLANKILLTFLEIMLVKMSLGMQY 625
QY 268 -VGLSLMD-----MTRM-----LNLIVFRFLIIPSKPMAVAVSTVLG 307
Db 626 FVSLFNRFQCFVYCGGIVELVLTSSKIMEPLGISVLRVRLRIEFTKSSMNSLSMLVAS 685
QY 308 LVONMRAFGIIVVY--YVFAIIGINLFRGYVALPGNSSILAPANGSAPGSEFQLEBY 364
Db 686 LMSIRSIASLVLFLFLFIIFALLCMQLEGGF-----SEIQEDK 727
QY 365 WANNFDPAALVTLNMLVAVNMWYF-----LDAYRRS--GPWSKIYFVLMVLSVYTW 418
Db 728 IRSNFTQIALTLFQIILTGDDWMEVYNGIEAVGASTIGLTSYFIVLFGNLYL 787
QY 419 VNLFLALLEN 429
Db 788 LNLFLAIVADN 798

```

RESULT 11

A54972

voltage-dependent calcium channel alpha 1E-3 - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999

C:Accession: A54972

R:Williams, M.E.; Marbidio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;

J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium chan

A:Reference number: A54972; MUID:94350992

A:Accession: A54972

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2270 <MTL>

A:Cross-references: GB:129385; NID:9495869; PIDN:AAA59205.1; PID:9495870

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match

Best Local Similarity 19.4%; Score 189; DB 2; Length 2270;

Matches 106; Conservative 91; Mismatches 218; Indels 132; Gaps 20;

```

QY 32 LMGDDPVVPMSCRRCSQDDGQD---RERLTYFQNLPESTLSLVLTTANNPDVWIPA 87
Db 259 LEQFDPPHPCGVQGPCGAYECKDWIGPNDDITQFDNIFAVLVFQCITMEGWTYLV--- 315
QY 88 YSKNRAYA-----IFFIVFTVIGSLFLMNLTLTAIYSQF-----RGYLMKSLQTS 132
Db 316 YNTNDALGATWMLKTFIPLIIGSFYVNLVGLVLSGEFAKERERVENRRRAFKLRQOO 375
QY 133 LFRRLCTRAFAEYVLSWGEAGAFPOATRNGPSTSLRRCRAPSSSATTTLTWTGTSNP 192
Db 376 IERELNGYRAMIDKAEVY-----LAEENKNACTSALEVLRATIRKSRTEATRTSSDPE 430
QY 193 W-----QTWCPFACSW-----WCMQMCCLISV--MTSS---WGFSTASLCT 229

```

```

Db 431 HCVDISVGTPLARASIKSAKVDGVSFRHKERLRIRISHHVKSQVFWIVSLVALNT 490
QY 230 TCWCCSRSLP-WACE-----GTCPTPACLTGSSPLSCMR-P 265
Db 491 ACVAIVHNPQWLTLLHYAEFLFLGLFLEMSLKMVGMPR---LYHSSPNCDFG 546
QY 266 EMWGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVSTVLGVQNMARAGTI 318
Db 547 VTGSIIEVVAIRPFGISFISVLRALRLRIKIKYMASSLNVLVSLMSKSIISL 606
QY 319 LVVWY---YVEAIGINLFRGVIALPGNSSLAPANGAPCGSEQLDEYMANDDPAA 375
Db 607 LFLFLFIVFALLGMQLFGGRFNFNDGTPSA-----NFDTPPA 646
QY 376 LVTLNMLAVVNM--OVFLDAYRRT---SGPWSKIYFVLMVLSVIVNLFALILENF 430
Db 647 IMTVFQILTGEDMNEVMYNGIRSGGVSSGMKSAIYFIVLTLFGNYTLNVLFLAIVDNL 706
QY 431 L-----HKMDPRSHLOPLAGTPPEATYQMYVLEFRDILEPGEDEL 471
Db 707 ANAQELTKDEEAEAFNQKHALQKAKVSPMSAPNMPISIERRRRHMSWEPSSHL 766
QY 472 TERLSOH 478
Db 767 RERRRRH 773

```

RESULT 12

S29237
 calcium channel protein BII-2, brain - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S29237
 R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
 FEBS Lett. 308, 7-13, 1992
 A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit
 A:Reference number: S29236; MUID:92354772
 A:Accession: S29237
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2178 <NII>
 A:Cross-references: EMBL:X67856; NID:q1474; PID:CAA48041.1; PID:q1475
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: transmembrane protein

Query Match 7.1%; Score 187; DB 2; Length 2178;

Best local similarity 18.1%; Pred. No. 1.1e-06; Indels 162; Gaps 18;

Matches 102; Conservative 91; Mismatches 207;

```

QY 32 LMGGDPVVPWSCRFCSQDDGOD---RERLTYFQNLPEISLTLVLTANNPDVMPA 87
Db 259 LEGDPPHPCGVGCGPAGYECKDMIGPNDGITQFDNLFVAVLVCQITWEGWTVL--- 315
QY 88 YSKNRAYA-----LEFIVTYIGSLFLMNLITAIYSQF-----RGYLMKSLQTS 132
Db 316 YNTNDALGATWNLVTFILIIIGSFVNLVGLVLSGEFAKEREKREVENRRAPFKLRQOQ 375
QY 133 LFRRLIGTAAFEVLSSVWEGGAFPOATRRGPSTSLFCRAPSSSATTTTLTWGTS 192
Db 376 IERELNGYRAWIDKAEVW-----LAENKNSGTSALEVLRRAITKRSRTAMTRDSSD- 429
QY 193 WQWCPFACSWCMQMCCLLSVMTSS----- 218
Db 430 -----EHCVDISSVGTPLARASIKSAKVDGASVFRHKERLRIRISVRAVKS 475
QY 219 ---WGSTASSLCTTCWCCSRSLP-WACE-----GTCPTPA 251
Db 476 QVFWIVSLVALNTPACVAIVHNPQWLTLLHYAEFLFLGLFLEMSLKMVGMPR-- 533
QY 252 TGLTSSPLSCMR-PEWGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVS 303
Db 534 --LYHSSPNCDFGVTSIFEVVAIRPFGISFISVLRALRLRIKIKYMASSLN 591

```

```

QY 304 TVLGVQNMARAGTILVWY---YVEAIGINLFRGVIALPGNSSLAPANGAPCGSFE 360
Db 592 LVVSLMSKSIISLFLFLFIVFALLGMQLFGGRNFNDGTPSA----- 638
QY 361 QLEYMANNEDDPAALVTLNMLVNNW--OVFLDAYRRT---SGPWSKIYFVLMVLS 415
Db 639 -----NFDTPPAIMTVFQILTGEDMNEVMYNGIRSGGVSSGMKSAIYFIVLTLFGN 691
QY 416 VIVWNLFLALILENLF-----HKMDPRSHLOPLAGTPPEATYQMYVE 456
Db 692 YTLNVLFLAIVDNLNANQELTKDEEAEAFNQKHALQKAEVSPMSAPNPIIERRR 751
QY 457 LIFRDLIEPGEDELTERLSOH 478
Db 752 RHHMSWEPSSHLRERRRRH 773

```

RESULT 13

S29236
 calcium channel protein BII-1, brain - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S29236
 R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
 FEBS Lett. 308, 7-13, 1992
 A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit
 A:Reference number: S29236; MUID:92354772
 A:Accession: S29236
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2253 <NII>
 A:Cross-references: EMBL:X67855; NID:q1472; PID:CAA48040.1; PID:q1473
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: transmembrane protein

Query Match 7.1%; Score 187; DB 2; Length 2259;

Best local similarity 18.1%; Pred. No. 1.1e-06; Indels 162; Gaps 18;

Matches 102; Conservative 91; Mismatches 207;

```

QY 32 LMGGDPVVPWSCRFCSQDDGOD---RERLTYFQNLPEISLTLVLTANNPDVMPA 87
Db 259 LEGDPPHPCGVGCGPAGYECKDMIGPNDGITQFDNLFVAVLVCQITWEGWTVL--- 315
QY 88 YSKNRAYA-----LEFIVTYIGSLFLMNLITAIYSQF-----RGYLMKSLQTS 132
Db 316 YNTNDALGATWNLVTFILIIIGSFVNLVGLVLSGEFAKEREKREVENRRAPFKLRQOQ 375
QY 133 LFRRLIGTAAFEVLSSVWEGGAFPOATRRGPSTSLFCRAPSSSATTTTLTWGTS 192
Db 376 IERELNGYRAWIDKAEVW-----LAENKNSGTSALEVLRRAITKRSRTAMTRDSSD- 429
QY 193 WQWCPFACSWCMQMCCLLSVMTSS----- 218
Db 430 -----EHCVDISSVGTPLARASIKSAKVDGASVFRHKERLRIRISVRAVKS 475
QY 219 ---WGSTASSLCTTCWCCSRSLP-WACE-----GTCPTPA 251
Db 476 QVFWIVSLVALNTPACVAIVHNPQWLTLLHYAEFLFLGLFLEMSLKMVGMPR-- 533
QY 252 TGLTSSPLSCMR-PEWGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVS 303
Db 534 --LYHSSPNCDFGVTSIFEVVAIRPFGISFISVLRALRLRIKIKYMASSLN 591
QY 304 TVLGVQNMARAGTILVWY---YVEAIGINLFRGVIALPGNSSLAPANGAPCGSFE 360
Db 592 LVVSLMSKSIISLFLFLFIVFALLGMQLFGGRNFNDGTPSA----- 638
QY 361 QLEYMANNEDDPAALVTLNMLVNNW--OVFLDAYRRT---SGPWSKIYFVLMVLS 415
Db 639 -----NFDTPPAIMTVFQILTGEDMNEVMYNGIRSGGVSSGMKSAIYFIVLTLFGN 691
QY 416 VIVWNLFLALILENLF-----HKMDPRSHLOPLAGTPPEATYQMYVE 456

```

Db 692 YTLINFLAIVADNLANAQELTKDEGEFAFNOKHLOKAKVSPKAPVNPSTERRR 751
 QY 457 LIFPDILPEEGDEBELTERLSQH 478
 Db 752 RHHMSWEPSSHLRERRRRH 773

RESULT 14

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C:Species: Homo sapiens (hmn)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999

C:Accession: B54972

R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; M.J.

J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A:Reference number: A54972; MUID:94350992

A:Accession: B54972

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-2251 <MIL>

A:Cross-references: GB:129384; NID:9495867; PIDN:AA59204.1; PID:9495868

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match

Best local similarity 7.1%; Score 186.5; DB 2; Length 2251;
 Best local similarity 20.5%; Pred. No. 1.2e-06;
 Matches 98; Conservative 84; Mismatches 184; Indels 113; Gaps 19;

QY 32 LMGDPVPVPSRCFSCQDDGOD---RERLTYFQNLPELSLTSLVLTANNPDVWIPA 87
 Db 259 LEEFDPHPGCGVCGAGYCKDMIGPDGITOEDNLFVAVLVFCITMEGTTVL--- 315
 QY 88 YSKNRVYA-----IEFIVTIGSLFLMNLTAIYSQF-----RGYLMKSLQTS 132
 Db 316 YNTNDALGATWMLYFIPILITIGSFVLNLVGLSEEFKEREVENRRAFMKLRQOQ 375
 QY 133 LERRRLGTRAAFEVLSSMVGEGAFPOATRRGPSTSLRFRAPSSSATITLTWTGSSP 192
 Db 376 IERELNGYRAWIDKAEVW-----LAEENKAGTSALEVARATIRKSRTEAMTRDSSDE 430
 QY 193 W-----QTMCPFACS-----WCWMOCCLISTV---WGSFTASSLCT 229
 Db 431 HCVDISSVGTPLARASIKAKVDGVSFRRKHERLIRISIHAWKSOVFYIVLSVALNT 490
 QY 230 TCWSCCSRLP-WACE-----GTCPPATCIGSSPLSCMR-P 265
 Db 491 ACVAIYHNHPQWLTLLTYAEFLGLFLLEMSLMTGMPR---LYFHSFNCDFDG 546
 QY 266 ENVGGL--SLMDKTRM-----LMLIVFRRLIIPMKRPAAVAVASTVLGIQNMRAFGI 318
 Db 547 VIVGSIFFEVWAIFFPGTSEGISLRLALRLRIFKITKWTASLRLNVLVSLMSMKSLISL 606
 QY 319 LVVVY---YVPAIIGINLFRGYVALPGSSSLAPANGSAPCGSEQLETWANNFDDPAAA 375
 Db 607 LFLFLFIVVFFALGMLQGLGGRFNENDGTPSA-----NFDFFPAA 646
 QY 376 LVTLMNLAVVNMW-OVFLDAYRY---SGPMKSIYFVLMVLVSSVIVWNLFLALLEN 429
 Db 647 IMTVFQILIGEDMNEVWYMGIRSGGVSSGMSAIFYIVLTFLGNTTLAVFLAIVDN 705

RESULT 15

A30063

dihydropyridine receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999

C:Accession: A30063

R:Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, V.; Takahashi, H.; Kangawa, K.; Koji

Nature 328, 313-318, 1987

A:Title: Primary structure of the receptor for calcium channel blockers from skeletal mu

A:Reference number: A30063; MUID:87258269

A:Accession: A30063

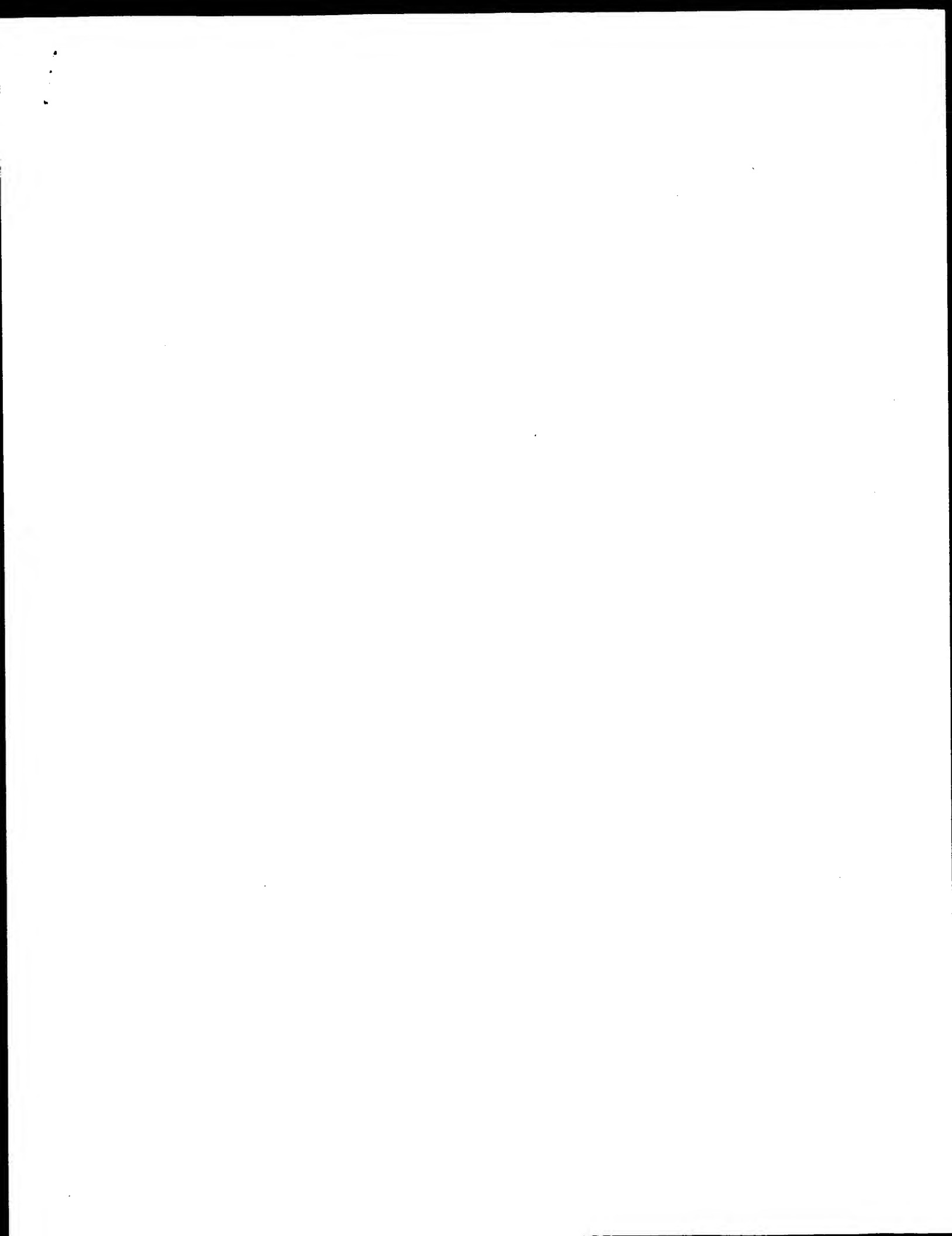
A:Molecule type: mRNA
 A:Residues: 1-1873 <TAN>
 A:Cross-references: GB:X05921; NID:91547; PIDN:CAA29355.1; PID:91548
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: phosphoprotein; transmembrane protein

Query Match

Best local similarity 7.1%; Score 186; DB 2; Length 1873;
 Best local similarity 18.1%; Pred. No. 1.1e-06;
 Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;

QY 58 LTVFQNLPELSLTSLVLTANNPDVWIPAYSKNRVYA-----IEFIVTIGSLFLMNL 112
 Db 272 ITHDNGFSLMIVYQCITMEGTTDVL---YVNDALGNEPMPWIFVYVLTLLGSSFFIILN 328
 QY 113 LTAIYSGFRGYLMKSLQTSLEFRRRLGTRAAFEVLSSWVG----- 152
 Db 329 VLGVLSEFTFERKRAKSRGTFQKLRKQLEEDLRGMSITGGEVMDVEDLRGKSL 388
 QY 153 -EGGAFPOATR--RGPSTSLRFRAPSSSATITLTWTGTSPPQW---CPFACS--- 202
 Db 389 EEGSDTESLYEIEGLNKIIQFIR-----HRRQNRVFRMKCHDLVK 430
 QY 203 ---WCWMOCC-----CLLSVMT-----SSWGFSTAS 225
 Db 431 SRVFWVLIVLVALNTLSIASHHNPPMLTHODIANRVLSLTLEMILMKYGLGRQ 490
 QY 226 SLCT-----TCWSCCSRLP-WACGTCPPATCIGSSPLSCMRPEWGLSLMDWTRM 279
 Db 491 YFMSIFNRFQCFVYVCSGILELLIVESGAMP---LGISVLRG----- 529
 QY 280 LNMIVFRRLIIPSMKRPAAVAVASTVLGIQNMRAFGILVVY---YVPAIIGINLFRG 336
 Db 530 -----IRLRLRLEKITWTSLSNLVSILNLSIRSLIASLTLFLFTIFALGMLQGLFG 583
 QY 337 VIVALPGNSSIAPANGSAPCGSEQLETWANNFDDFAALVTLNMLAVVNMW-OVFLDAY 395
 Db 584 RY-----DFEDTEVRKSNPNFQALISVQVLTGEDMNSVMYNGI 624
 QY 396 RRTSGPMSK---YFVLMVLVSSVIVWNLFLALILENPLH-----KWDPRSHT 440
 Db 625 MAYGGEPSGVLCIYFIILFVCGNYTLNVLAVDNLAESAISLQAQAKAEERKR 684
 QY 441 OPLAGPEATQYQWVELLFRLDILPEEGDEBELTERLSQH 479
 Db 685 KMSRGLPDKT-----EEKSYWAKKLEQKP 709

Search completed: October 8, 2002, 10:06:01
 Job time : 47 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:08:41 ; Search time 25 Seconds

(without alignments)
751.159 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634
Sequence: 1 MSSACWEATGRCRLGGGMV.....PGEDELTERLSQHPHMLWLCR 485

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	7.6	2190	1	CCAD_CHICK
2	196	7.4	2169	1	CCAC_RAT
3	194	7.4	2222	1	CCAE_RAT
4	194	7.4	2272	1	CCAE_MOUSE
5	191	7.3	2312	1	CCAE_HUMAN
6	190	7.2	1610	1	CCAD_MESAU
7	189.5	7.2	2223	1	CCAE_DISOM
8	187.5	7.1	1966	1	CCAF_HUMAN
9	187	7.1	2161	1	CCAD_HUMAN
10	187	7.1	2259	1	CCAE_RABIT
11	186	7.1	1873	1	CCAS_RABIT
12	184	7.0	1873	1	CCAS_HUMAN
13	184	7.0	2221	1	CCAC_HUMAN
14	182	6.9	2339	1	CCAB_HUMAN
15	179.5	6.8	2171	1	CCAC_RABIT
16	178.5	6.8	2203	1	CCAD_RAT
17	177	6.7	2139	1	CCAC_MOUSE
18	175.5	6.7	2339	1	CCAB_HUMAN
19	175.5	6.7	2353	1	CCAB_HUMAN
20	171	6.5	2254	1	CCAG_HUMAN
21	171	6.5	2377	1	CCAG_HUMAN
22	170.5	6.5	1835	1	CCAI_RAT
23	169.5	6.4	2505	1	CCAA_HUMAN
24	168	6.4	2336	1	CCAB_RAT
25	167.5	6.4	2164	1	CCAA_MOUSE
26	165.5	6.3	2327	1	CCAB_MOUSE
27	164.5	6.2	2424	1	CCAB_RABIT
28	163.5	6.2	1687	1	CCAM_MOUSE
29	163	6.2	1852	1	CCAS_MOUSE
30	160.5	6.1	2212	1	CCAA_RAT
31	160	6.1	1951	1	CIN3_HUMAN
32	159.5	6.1	2019	1	CIN3_RAT
33	159	6.0	1951	1	CIN3_RAT

34	155.5	5.9	2516	1	CCAD_DROME	Q24270 drosophila
35	154.5	5.9	2016	1	CIN5_HUMAN	Q14524 homo sapien
36	148.5	5.6	1820	1	CINA_ELEEL	P02719 electrophor
37	148	5.6	2326	1	CCAB_DISOM	P56698 discoppyge o
38	146	5.5	2131	1	CINA_DROME	P35300 drosophila
39	145.5	5.5	1848	1	CCAA_DROME	P91645 drosophila
40	145	5.5	2009	1	CIN1_HUMAN	P35498 homo sapien
41	145	5.5	2039	1	CCH1_YEAST	P50077 saccharomyc
42	144.5	5.5	2009	1	CIN1_RAT	P04774 rattus norv
43	142.5	5.4	2005	1	CIN2_RAT	P04775 rattus norv
44	142	5.4	1836	1	CIN4_HUMAN	P35499 homo sapien
45	139	5.3	1146	1	CCAS_RAT	Q02485 rattus norv

ALIGNMENTS

RESULT 1
ID CCAD_CHICK STANDARD: PRT; 2190 AA.
AC 073700: 073701: 073702: 073703: 073704:
DT 15-JUL-1999 (Rel. 38, created)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 30-MAY-2000 (Rel. 39, last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit
DE (CHCAHALD).
GN CACNALD
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98070847; PubMed=9405708;
RA Kollmar R., Montgomery L.G., Fak J., Henry L.J., Hudspeith A.J.;
RT "Predominance of the alpha1D subunit in L-type voltage-gated Ca²⁺
RT channels of hair cells in the chicken's cochlea."
RL Proc. Natl. Acad. Sci. U.S.A. 94:14883-14888(1997).
[2]
ALTERNATIVE SPLICING.
RP MEDLINE=98070848; PubMed=9405709;
RX Kollmar R., Fak J., Montgomery L.G., Hudspeith A.J.;
RT "Hair cell-specific splicing of mRNA for the alpha1D subunit of
RT voltage-gated Ca²⁺ channels in the chicken's cochlea."
RL Proc. Natl. Acad. Sci. U.S.A. 94:14889-14893(1997).
CC -1- FUNCTION: THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM
CC CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE
CC "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP.
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: MANY VARIANTS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE BASILAR PAPILLA OF THE
CC COCHLEA.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.

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FT	REPEAT	108	404	I.
FT	REPEAT	530	776	II.
FT	REPEAT	894	1176	III.
FT	REPEAT	1213	1496	IV.
FT	DOMAIN	1	121	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	122	140	S1 OF REPEAT I (POTENTIAL).
FT	DOMAIN	141	158	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	159	178	S2 OF REPEAT I (POTENTIAL).
FT	DOMAIN	179	190	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	191	209	S3 OF REPEAT I (POTENTIAL).
FT	DOMAIN	210	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	231	249	S4 OF REPEAT I (POTENTIAL).
FT	DOMAIN	250	268	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	269	288	S5 OF REPEAT I (POTENTIAL).
FT	DOMAIN	289	376	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	377	401	S6 OF REPEAT I (POTENTIAL).
FT	DOMAIN	402	544	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	545	564	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	565	579	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	580	598	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	599	606	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	607	625	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	626	635	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	636	654	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	655	673	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	674	694	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	695	748	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	749	773	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	774	907	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	908	926	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	927	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	943	962	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	963	974	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	975	993	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	994	999	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	1000	1019	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1020	1038	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	1039	1058	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1059	1148	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	1149	1169	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1170	1226	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	1227	1245	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1246	1260	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	1261	1280	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1281	1297	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	1298	1319	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1320	1342	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	1343	1362	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1363	1381	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	1382	1401	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1402	1468	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	1469	1493	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1494	2190	CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	5	8	POLY-GLN.
FT	DOMAIN	674	680	POLY-LEU.
FT	DOMAIN	1154	1160	POLY-IIE.
FT	DOMAIN	1703	1706	POLY-GLU.
FT	DOMAIN	424	441	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	359	359	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	726	726	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1122	1122	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1435	1435	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	BINDING	1096	1186	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1449	1515	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1461	1504	TO PHENYLALKYLAMINES (BY SIMILARITY).
FT	MOD_RES	1504	1504	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1522	1533	POTENTIAL.
FT	CARBOHYD	324	324	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	150	150	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	459	484	MISSING (IN ISOFORM I-II-LOOP).
FT	VARSPLIC	939	958	ILGADVETSEMFETLIK -> ILGDFAFALFVETL LK (IN ISOFORM IIIS2).
FT	VARSPLIC	1284	1293	MISSING (IN ISOFORM IVS2-IVS3).
FT	VARSPLIC	1294	1321	GYFSDAMTFSLVIGSIVDVLSAD -> HYTFDAMT FDLVIGSVVDIAETVEN (IN ISOFORM IVS3).
FT	VARSPLIC	1671	1705	AGLTLHIGELIRRAISCDDODEPEENPDEE -> VL IAHRAOPFCSPASKLPFGAEMVLQRAQVA (IN CLONE PSE29/31-2).
FT	VARSPLIC	1706	2190	MISSING (IN CLONE PSE29/31-2).
FT	VARSPLIC	1710	1728	RNGALFGHNIHISDRD -> VMSEHGIVFLCNMSFI E (IN CLONE PSE29/31-1).
FT	VARSPLIC	1729	2190	MISSING (IN CLONE PSE29/31-1).
FT	VARSPLIC	1892	1894	HVY -> NGP (IN CLONE PSE48/154-1).
FT	VARSPLIC	1895	2190	MISSING (IN CLONE PSE48/154-1).
SO	SEQUENCE	2190 AA;	249342 MW;	10680CICB7708651 CRC64;
Query Match				
Best Local Similarity 7.6%, Score 200; DB 1; Length 2190;				
Matches 95; Conservative 18.1%; Pred. No. 9.1e-08;				
Matches 95; Conservative 164; Mismatches 164; Indels 188; Gaps 16;				
OY	16	GGMMVPTGVNRLELSLWGGDPVVPWSCRFCSQDDGDRERLTYFONLPESITSLVL	75	
DB	330	GGWVBPNGCI	356	
OY	76	TTANPDVIMPAYSKRNRAVA	121	
DB	357	TMEGWTDLV	413	
OY	122		130	
DB	414	RGDFQKLEKQOLEBDLKGIDWITQOEDIDPENDEADEBGRNNRVTLADIEMKKNSR	473	
OY	131	TSLFRRRLGTRAFEEV	168	
DB	474	LSCFRRSSNKAHSMPTSETESYNTENVSAGEGNPACCSLOTISKNSPSSRRMRNNFN	533	
OY	169	LRFGRAPSSSSA	214	
DB	534	RKCKAAAVKSVTFYVLVIVLFLNLTLTISSEHYNOPDMLTQIODANRYLLALFTCEMLV	593	
OY	215	MTSMSGFSTASSLCYTCSCCSRSJPMWACEGCPPARCTIGSSPLSCMRPEMGLSLM	274	
DB	594	KMTSLGLDAIYFVSLNRPDCFY	635	
OY	275	DMTRLMLLVEFLRLIIPSMKPAVVAIVSLGIVQNNAFGLLVVY	331	
DB	636	ISVFRVRLIRIKFVTRHMASLSTLVASLNSKMSIASLTLFLFIIFISLGM	690	
OY	332	NLFREVYALPONSLSLAFANGSAPCGSPFOLEYMANNDPFAALVITLMLNLYVNNQV	390	
DB	691	QLFGRKF	731	

QY 391 FLDAVRRYSGPMGR-----IYFVLMVLVSSVIVNLFALILEN 429
 Db 732 MYGIMAYGSPSSGMIVCITIFITLFCGMYILLNVLAVDN 775

RESULT 2
 CCAC RAT STANDARD: PRT: 2169 RA
 AC P22002: P27733; P27734; Q62816; Q63271; Q64178;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1C subunit (calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (RAT brain class C) (RBC)
 GN CACNA1C OR CACNA1A1 OR CCHL1A1 OR CACH2 OR CACN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (CARDIAC ISOFORM S3B).
 RC TISSUE-Aorta;
 RX MEDLINE-91009241; PubMed-2170396;
 RA Koch W.J., Ellinor P.T., Schwartz A.;
 RT "cDNA cloning of a dihydropyridine-sensitive calcium channel from rat aorta. Evidence for the existence of alternatively spliced forms.";
 RL J. Biol. Chem. 265:17786-17791(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS RBC-I AND RBC-II).
 RC TISSUE-Brain;
 RX MEDLINE-91299339; PubMed-1648941;
 RA Snutch T.P., Tomlinson W.J., Leonard J.P., Gilbert M.M.;
 RT "Distinct calcium channels are generated by alternative splicing and are differentially expressed in the mammalian CNS.";
 RL Neuron 7:45-57(1991).
 RN [3]
 RP SEQUENCE OF 1168-1413 FROM N.A. (CLONE RBC-61).
 RX MEDLINE-90239020; PubMed-1692134;
 RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
 RT "Rat brain expresses a heterogeneous family of calcium channels.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
 RN [4]
 RP SEQUENCE OF 1269-1415 FROM N.A. (ISOFORMS S3A; S3B AND DELETED D1).
 RX MEDLINE-92159076; PubMed-1311102;
 RA Diebold R.J., Koch W.J., Ellinor P.T., Wang J.-J., Mutchamy M., Wiczonek D.F., Schwartz A.;
 RT "Mutually exclusive exon splicing of the cardiac calcium channel at subunit generates developmentally regulated isoforms in the rat heart.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1497-1501(1992).
 RN [5]
 RP SEQUENCE OF 1269-1387 FROM N.A.
 RC TISSUE-Myometrium;
 RX MEDLINE-96043375; PubMed-7485440;
 RA Tezuka N., Ali M., Chwalisz K., Garfield R.E.;
 RT "Changes in transcripts encoding calcium channel subunits of rat myometrium during pregnancy.";
 RL Am. J. Physiol. 269:C1008-C1017(1995).
 RN [6]
 RP SEQUENCE OF 1202-1495 FROM N.A. (ISOFORM DELETED D1 FORK/ROB2).
 RC TISSUE-Osteosarcoma;
 RX MEDLINE-96074617; PubMed-4479909;
 RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;
 RT "Multiple calcium channel transcripts in rat osteosarcoma cells: selective activation of alpha 1D isoform by parathyroid hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE-93374932; PubMed-8396138;
 RA Hell J.W., Yokoyama C.T., Wong S.T., Warner C., Snutch T.P., Caterall W.A.;

RT "Differential phosphorylation of two size forms of the neuronal class C L-type calcium channel alpha 1 subunit.";
 RL J. Biol. Chem. 268:19451-19457(1993).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP) AND PHENYLALANINES, BENZOTRIAZEPINES, AND BY OMEGA-AGATOXIN-111A (OMEGA-AGA-111A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC S3A, CARDIAC ADULT ISOFORM S3B (SHOWN HERE), CARDIAC DELETED D1 FORM/ROB2, BRAIN ISOFORM RBC-I AND BRAIN ISOFORM RBC-II; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: RBC-I AND RBC-II ARE EXPRESSED THROUGHOUT THE CENTRAL NERVOUS SYSTEM, WITH HIGHEST LEVELS IN OLFACTORY BULB AND CEREBELLUM. ALSO EXPRESSED IN HEART, PITUITARY, ADRENAL GLAND, LIVER, KIDNEY, AND IN A MUCH LESSER EXTENT IN TESTES AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM EMBRYONIC DAY 16 THROUGHOUT THE ADULT.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF INHIBITS THE OPENING OF THE CHANNEL (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATION BY CAK ACTIVATES THE CHANNEL (PROBABLE). IS ALSO PHOSPHORYLATED IN VITRO BY CAM-KINASE II, PKC AND GSKP.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
 CC -----
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 CC -----
 CC EMBL: M59786; AAA85463.1; -
 CC EMBL: M67515; AAA18905.1; -
 CC EMBL: M67516; AAA42016.1; -
 CC EMBL: M91242; AAA41460.1; -
 CC EMBL: M91240; AAA41460.1; JOINED.
 CC EMBL: M89924; AAA41460.1; JOINED.
 CC EMBL: M91241; AAA41460.1; JOINED.
 CC EMBL: S80558; AAB35528.1; -
 CC EMBL: U31815; AAA89157.1; -
 CC InterPro: IPR002077; Ca_channel.
 CC InterPro: IPR002111; Cal_channel_Tryp.
 CC InterPro: IPR000636; Cation_chan_non_lig.
 CC InterPro: IPR001882; Channel_pore_Ca_Na.
 CC Pfam: PF00520; Ion_trans_4.
 CC PRINTS: PR00167; CACHANNEL.
 CC DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; Alternative splicing.
 CC REPEAT 141 438 1.

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FT REPEAT 540 786 II.
FT REPEAT 917 1198 III.
FT REPEAT 1235 1508 IV.
FT DOMAIN 1 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 173 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 174 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 211 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 212 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 242 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 243 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 281 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 282 300 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 301 320 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 321 410 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 411 435 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 436 554 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 555 573 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 574 588 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 589 608 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 609 616 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 617 635 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 636 645 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 646 664 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 665 683 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 684 703 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 704 758 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 759 783 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 784 930 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 931 949 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 950 965 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 966 985 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 986 997 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 998 1016 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 1017 1023 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1024 1041 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1042 1060 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1061 1080 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1081 1170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1171 1195 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1196 1248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1249 1267 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1268 1282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1283 1302 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1303 1310 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1311 1329 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1330 1353 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1354 1372 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1373 1391 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1392 1411 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1412 1480 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1481 1505 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1506 2169 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2169 475 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT DOMAIN 684 690 POLY-LEU.
FT DOMAIN 798 804 POLY-GLU.
FT DOMAIN 1176 1182 POLY-ILE.
FT SITE 393 393 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 736 736 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1116 1116 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

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Query Match
Best Local Similarity 19.3%; Score 196; DB 1; Length 2169;
Matches 104; Conservative 83; Mismatches 172; Indels 180; Gaps 22;

QY 46 CSQDGDGQDERLTYFQNPESITSLVLTANPDVMIPTAKRAYA-----LEFLY 100
DB 362 CKRGWDG-PKHGITNEDNFAMLTVEQCITMGWTDVL---YMODAGYELPWVYFS 417
QY 101 FTYIGSLFNLNLTATYISF-----RGTL----- 125

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DB 418 LVYFGSEFVLNLVGLVSGEFSKEREKAKRGDFOKLRKQOLEDJLGYIDMTIQAEDI 477
QY 126 -----MKSLQTS-----LFRRRLGTRAAEVLSSWVEGGA 156
DB 478 DPENEDEGDEKPRMMSPTSETESVNTENVAGGIBEGNCARLARHSKS-----K 531
QY 157 FPGATRGSTSLRFGCRAPSSSA-----TTLTITWGTSPP-WQWCFACSW 203
DB 532 FSRYMRMRNRCRCRAAVKSNVEFWLVIFLVNLTITIASEHNQPMWLEVDOTAN- 590
QY 204 CWMQKCLISVYMS-----SMGFSASSICCTTCMSSCSRLPMAECGTCTPATCLTG 256
DB 591 -----KALLALEFEMLMKMSYGLQATVYSLNFRDCI-----VCGIITLIVERKI 640
QY 257 SSPV--SCWRPEVYGLSLMDTMRMLIVERFLRIPSCKMAVAVSTVLGLVQNMRA 314
DB 641 MSPLGISCMR--CVRLRLRIFKIRYWNLS-----SNLVASLINSLSRS 680
QY 315 FGGILVVY---YVPAIIGINLFRGYVALPQNSLAPANGSAPGSGFQLEVMANNPDD 371
DB 681 IASILLFLFLFIIFSLGMOLEGRF-----NFDEMOTRSTFDN 721
QY 372 FAALVTITMLVYNNW-QVELDAYRRYSGPMCK-----IFYLWMLVSSVIVMLFLAL 425
DB 722 FPGSLTFVQILGEDMSVMTGCIATYGGSPRGMVLCIFYLFIISPNTILNLFAL 781
QY 426 ILENFL-----HKMDPRSHLOPLAGT--DEATYQMTVELLPDILPEGEDELTE 473
DB 782 AVDLMAESLTSQKREERKRLATFASPEKR-----QEVMEKPAVERSK 831

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RESULT 3
ID CCAL_RAT STANDARD; PRT; 2222 AA.
AC 007652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (RBE-IT) (RBE2)
DE (Brain calcium channel II) (BII).
DE CACNA1E OR CACNA1A6 OR CACNA6.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=93262464; PubMed=8386125;
RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
RA Sautch T.P.;
RT "Structure and functional expression of a member of the low voltage-activated calcium channel family.";
RT Science 260:1133-1136(1993).
RL -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP). OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA), CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.
CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM

CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
 CC INSULINOMA.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: L15453; AAA40855.1; -
 CC InterPro: IPR002077; Ca_channel.
 CC InterPro: IPR002111; Cat_channel_TrpL.
 CC InterPro: IPR000636; Cation_chan_non_11g.
 CC InterPro: IPR001682; Channel_pore_Ca_Na.
 CC Pfam: PF00520; Ion_trans; 4.
 CC PRINTS: PR00167; CACHANNEL.
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;
 CC Calcium-binding; Phosphorylation.
 CC REPEAT 27 305
 CC REPEAT 413 657
 CC REPEAT 1092 1378
 CC REPEAT 1415 1678
 CC DOMAIN 1 40
 CC TRANSMEM 41 59
 CC TRANSMEM 60 78
 CC TRANSMEM 79 97
 CC TRANSMEM 98 109
 CC TRANSMEM 110 124
 CC TRANSMEM 125 136
 CC TRANSMEM 137 156
 CC TRANSMEM 157 174
 CC TRANSMEM 175 195
 CC TRANSMEM 196 277
 CC TRANSMEM 278 301
 CC TRANSMEM 302 427
 CC TRANSMEM 428 447
 CC TRANSMEM 448 460
 CC TRANSMEM 461 480
 CC TRANSMEM 481 489
 CC TRANSMEM 490 508
 CC TRANSMEM 509 518
 CC TRANSMEM 519 537
 CC TRANSMEM 538 556
 CC TRANSMEM 557 576
 CC TRANSMEM 577 629
 CC TRANSMEM 630 654
 CC TRANSMEM 655 1100
 CC TRANSMEM 1101 1117
 CC TRANSMEM 1118 1141
 CC TRANSMEM 1142 1161
 CC TRANSMEM 1162 1169
 CC TRANSMEM 1170 1192
 CC TRANSMEM 1193 1206
 CC TRANSMEM 1207 1224
 CC TRANSMEM 1225 1243
 CC TRANSMEM 1244 1263
 CC TRANSMEM 1264 1350
 CC TRANSMEM 1351 1374
 CC TRANSMEM 1375 1431
 CC TRANSMEM 1432 1450

FT DOMAIN 1451 1467
 FT TRANSMEM 1468 1485
 FT DOMAIN 1486 1493
 FT TRANSMEM 1494 1512
 FT DOMAIN 1513 1523
 FT TRANSMEM 1524 1542
 FT DOMAIN 1543 1561
 FT TRANSMEM 1562 1581
 FT DOMAIN 1582 1650
 FT TRANSMEM 1651 1676
 FT DOMAIN 1677 2222
 FT TRANSMEM 667 672
 FT DOMAIN 699 704
 FT TRANSMEM 718 723
 FT DOMAIN 1058 1064
 FT TRANSMEM 1180 1183
 FT DOMAIN 2193 2196
 FT TRANSMEM 325 342
 FT SITE 260 260
 FT SITE 608 608
 FT SITE 1324 1324
 FT SITE 1615 1615
 FT CA_BIND 377 388
 FT MOD_RES 1686 1686
 FT CA_BIND 1704 1715
 FT CARBOHYD 205 205
 FT CARBOHYD 1518 1518
 FT CARBOHYD 1523 1523
 FT CARBOHYD 1641 1641
 FT CARBOHYD 2222 AA; 252114 MW; DF6452A217CEB19 CRC64;
 SQ SEQUENCE
 Query Match 7.4%; Score 194; DB 1; Length 2222;
 Best Local Similarity 20.8%; Pred. No. 2,7e-07;
 Matches 113; Conservative 86; Mismatches 221; Indels 122; Gaps 21;
 QY 32 LMGDPVWVWSCRFSGQDDGD---REKLYFQNLPSLSLVLTTANNPDVMPA 87
 DB 210 LGEFDPHPGCGVGGCAGYCKMDWIPNDITQFDNLFAVLVFCIMEGWTVL--- 266
 QY 88 YSKNRVYA-----IEFIVTVGSLFNMNLTAIITSQF-----RGYLMKSLQTS 132
 DB 267 YINNDLGGATWMLYFTPLITIGSFVLNVLGVLSGEFAKEREVENRRRAFKLRQOO 326
 QY 133 LFRRLGTRP---AFEVL--SSMWGEAGAFQATRRGPSTSLR--FCRAPSSSATTTL 184
 DB 327 IERELNGYRAMIDKAEEVWLAENKNKSGTSALEVLRAATIKRRTAMKRDSSDEHCYVI 386
 QY 185 TTWGT---SSPMQWCPAPSCMCMQCCLSV--MTSS---WGFSTASSICTTCWSC 234
 DB 387 SSVGTPLARASIKSTKVDASVFRHKERLIRISIRHNVKSQVYVIVLSVALINTACVAI 446
 QY 235 GSRSLP-NACE-----GTCPTATCTGSSPLSCMR-PEMWGL 270
 DB 447 VHHNDOPWLTLLIYLAEPFLGLFLEMGLKMYGMGP---LYFHSFNCDFGVTVGS 502
 QY 271 L--SLMDWTRM-----LNNLIVFERFLRIPSKMPAAVAVSTVLGYONRRAGGILVVY 323
 DB 503 IFEVVAWIRPETSIGISVLRALRLRIKIKYASLNLVSLMSKSKSIISLFLIF 562
 QY 324 ---YFPAITIGLPLFGVIALPFGNSLAPANGSAPCGSFQOLEYMANNFDEPAALVITM 380
 DB 563 LFTVVFALIGMLFGFGRENFNDGTPSA-----NEDTPEPAIMTVF 602
 QY 381 NLMVAVNNM--QVLDLAVRR---SGPMKITYVLMWIVSVIWMVNLATLLENFL--- 431
 DB 603 QITLEDNNEVWYNGIRSGGVSSGMSVITVITLFGENTVLVLAIVADNLANNOE 662
 QY 432 -----HKWDPKSHLOPLAGTPREATYOMTELLFRDILPEEGDELETERLS 476

FT SITE 658 658 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 FT SITE 1375 1375 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 FT SITE 1666 1666 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 FT CA_BIND 427 438 BY SIMILARITY.
 FT MOD_RES 1737 1737 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CA_BIND 1755 1766 BY SIMILARITY.
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1569 1569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1692 1692 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2272 AA; 257233 MW; 70D920B9E0C87A1 CRC64;

Query Match 7.4%; Score 194; DB 1; Length 2272;
 Best Local Similarity 20.8%; Pred. No. 2.8e-07;
 Matches 113; Conservative 86; Mismatches 221; Indels 122; Gaps 21;

32 LMGDPVYVWSCRFGSQDDGOD---RRRLTYFQNLPSLTSLLVLTANNPDVYIPA 87
 260 LGGFPPHPCGVGCPAGYECKDMIGPNDGITOQDNILFAVLTFQCTMEGWTVL--- 316
 88 YSKNRYA-----IFPIYTVIGSLFIMNLITALLIYSOP-----RGYLMKSLQTS 132
 317 YTNMDALGATWMLVTFPIITIGSFVLNVGVLGSEFAKEREVENRAFKRLRQOO 376
 133 LERRRLGTRA---AFEVL--SSMVEGGAFFQATRRGPSTSLR--FCRAPSSSATVTL 184
 377 IRRRLNGYRAWIDKAEVLAENKNSGTSALEVLRATIKRSRTAMRDSDELCYVI 436
 165 TTWGT---SSPWQWCPFACSCWCMQCLISV--MISS---WGSTASSICTTCWSC 234
 437 SSVGTPILARASIKSTKYDCASTYRKRERLLRISIRHMVKSQVYVTVLSVALNTACVAI 496
 235 CSRSIP-WACE-----GTCPTPATLUTGSSPSLSCAR-PEMVG 270
 497 VHHNPQWHLTHLYAEPFLCFLLEMSLKMYGMGR---LYRHSNCFDEGVTS 552
 271 L--SLMDMTRM-----LNMILVERFLRITPSKPMVAVSTVGLVQNNRAGGILVVY 323
 553 IFEVVAITRPCTSGISVLRALRLRIKTKYMASLNLVVSLSMSKSIISLFLLF 612
 324 ---YVFAITIGLFGVIALVGLNGSSSLAPANGSAPCGSEGLEEYANNFDDFAALVTIM 380
 613 LEIVFALLGMQLFGGRENFDGTPSA-----NEDTPEPALIMTVF 652
 381 NLMVNNM--QVPLDAYRRY---SGPWSKIYFVLMVLYSSVAVNMLFALLILENL---- 431
 653 QILTGEDMNEVWYNGIRSGGVSSGMSAITYIVTLFGNTYLLNVLAIADVNANAOE 712
 432 -----HKWDPRSHLOPLAGTPREATYQMTVELFRDILLEPGEDELTERLS 476
 713 LTKDQEEAEAFNOKHALOKAKEVSPMASPNPSTIERDRRRHHHMSMWRPSSHILRRRR 772
 477 OH 478
 773 RH 774

RESULT 5

CCAE_HUMAN STANDARD: PRT; 2312 AA.
 ID CAE_HUMAN
 AC Q15878; Q14581; Q14580;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium
 channel, L type, alpha-1 polypeptide, Isoform 6) (Brain calcium
 channel II) (B11).
 GN CACNA1E OR CACNA1A6 OR CACN6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=95236033; PubMed=7536609;
 RA Schneider T., Wei X., Olcese R., Costantin J.L., Neely A., Palade P.,
 RA Perez-Reyes E., Qin N., Zhou J., Crawford G.D., Smith R.G.,
 RA Appel S.H., Stefani E., Birnbaumer M.;
 RT "Molecular analysis and functional expression of the human type E
 RT neuronal Ca2+ channel alpha 1 subunit.";
 RL Recept. Channels 2:255-270(1994).
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hippocampus;
 RX MEDLINE=94350992; PubMed=8071363;
 RA Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F.,
 RA Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
 RT "Structure and functional characterization of neuronal alpha 1E
 RT calcium channel subtypes.";
 RL J. Biol. Chem. 269:22347-22357(1994).
 CC - FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
 CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
 CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA).
 CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPIRIDINES (DHP), OMEGA-
 CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
 CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
 CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
 CC IMPORTANT FOR INFORMATION PROCESSING.
 CC - SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-1E-1 AND ALPHA-1E-3
 CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC - TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES AND IN KIDNEY.
 CC - DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC - SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC
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 CC
 CC EMBL: L27745; AAA72125.1; -;
 CC EMBL: L29384; AAA59204.1; -;
 CC EMBL: L29385; AAA59205.1; -;
 CC MIM: 601013; -;
 CC InterPro: IPR002077; Ca_channel.
 CC InterPro: IPR002111; Ca_channel_TripL.
 CC InterPro: IPR000636; Cation_chan_non_lig.
 CC InterPro: IPR001682; Channel_pore_Ca_Na.
 CC Pfam: PF00520; Ion_trans_4.
 CC PRINTS: PR00167; CACHANNEL.
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;
 CC Calcium-binding; Phosphorylation; Alternative splicing.

FT REPEAT 76 354 I (BY SIMILARITY).
 FT REPEAT 462 706 II (BY SIMILARITY).
 FT REPEAT 1139 1425 III (BY SIMILARITY).
 FT REPEAT 1462 1725 IV (BY SIMILARITY).
 FT DOMAIN 1 89 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 90 108 S1 OF REPEAT I.
 FT DOMAIN 109 127 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 128 146 S2 OF REPEAT I.
 FT DOMAIN 147 158 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 159 173 S3 OF REPEAT I.
 FT DOMAIN 174 185 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 186 205 S4 OF REPEAT I.
 FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 224 244 S5 OF REPEAT I.
 FT DOMAIN 245 326 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 327 350 S6 OF REPEAT I.
 FT DOMAIN 351 476 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 477 496 S1 OF REPEAT II.
 FT DOMAIN 497 509 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 510 529 S2 OF REPEAT II.
 FT DOMAIN 530 558 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 557 567 S3 OF REPEAT II.
 FT DOMAIN 568 605 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 606 625 S4 OF REPEAT II.
 FT DOMAIN 626 678 S5 OF REPEAT II.
 FT DOMAIN 679 703 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 704 1147 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1148 1164 S1 OF REPEAT III.
 FT DOMAIN 1165 1188 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1189 1208 S2 OF REPEAT III.
 FT DOMAIN 1209 1216 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1217 1239 S3 OF REPEAT III.
 FT DOMAIN 1240 1253 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1271 1271 S4 OF REPEAT III.
 FT DOMAIN 1272 1290 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1291 1310 S5 OF REPEAT III.
 FT DOMAIN 1311 1397 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1398 1421 S6 OF REPEAT III.
 FT DOMAIN 1422 1478 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1479 1497 S1 OF REPEAT IV.
 FT DOMAIN 1498 1512 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1513 1532 S2 OF REPEAT IV.
 FT DOMAIN 1533 1540 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1541 1559 S3 OF REPEAT IV.
 FT DOMAIN 1560 1570 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1571 1589 S4 OF REPEAT IV.
 FT DOMAIN 1590 1608 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1609 1628 S5 OF REPEAT IV.
 FT DOMAIN 1629 1697 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1698 1723 S6 OF REPEAT IV.
 FT DOMAIN 1724 2312 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 716 721 POLY-GLU.
 FT DOMAIN 748 753 POLY-ARG.
 FT DOMAIN 767 772 POLY-ARG.
 FT DOMAIN 1227 1230 POLY-VAL.
 FT DOMAIN 2283 2287 POLY-ARG.
 FT DOMAIN 374 391 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
 FT SITE 309 309 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 657 657 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1371 1371 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1662 1662 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1662 1662 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT CA_BIND 426 437 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CA_BIND 1733 1733 BY SIMILARITY.
 FT CA_BIND 1751 1762 BY SIMILARITY.
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1565 1565 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1570 1570 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 748 766 MISSING (IN ISOFORM ALPHA-1E-1).
 FT CONFLICT 648 648 I -> M (IN REF. 2).
 FT CONFLICT 836 837 WP -> LAL (IN REF. 2).
 FT CONFLICT 1954 1954 T -> A (IN REF. 2).
 FT CONFLICT 1954 1954 MISSING (IN REF. 2).
 FT CONFLICT 1966 2008 MISSING (IN REF. 2).
 FT CONFLICT 2076 2076 R -> P (IN REF. 2).
 FT CONFLICT 2083 2083 G -> R (IN REF. 2).
 FT CONFLICT 2205 2205 C -> W (IN REF. 2).
 FT CONFLICT 2218 2218 S -> W (IN REF. 2).
 FT CONFLICT 2244 2244 G -> V (IN REF. 2).
 FT SEQUENCE 2312 AA; 261727 MW; 633ED3EFD407D63E CRC64;
 Query Match 7.3%; Score 191; DB 1; length 2312;
 Best local similarity 19.4%; Pred. No. 4.9e-07;
 Matches 106; Conservative 91; Mismatches 218; Indels 132; Gaps 20;
 QY 32 LMGDDPVWPCSCFSCQDDGDQD---REKLYTFQNLPELSLTLVLTANNPDVWIPA 87
 DB LFGFDPHPGCGVCGPAGYCKDKMIGPNDIGTFQNLPELTLVTFQCLTEGWTTLV--- 315
 QY 88 YSKNRAYA-----IEFTVTVIGSLFLMNLTLTAIYSQF-----RGYLMKSLQTS 132
 DB YNTNDALGATWMLDYFPLIITISFVLNLVGLSGEFAKEREVRNRRAPKLRQOQ 375
 QY 133 LFRRLRTRAAFELSSVMGEGAFPOATRRGPSTSLRCRAPSSSATTTLTWTGSSP 192
 DB IERELNGYRAMIDKAEVW-----LAENKNAGTSALVLRRAIKRSFTEAMTROSSDE 430
 QY 193 W-----QTCPPFACS-----WCWMQCCLLSV--MSS-----WGFSTASSLCT 229
 DB HCYDVISVGTPLARASIKSAKVDGVSYFRHKERLLRISIHMKSOQFYIVLVALNT 490
 QY 230 TCWSSCSRSLP-NACE-----GTCPTPATCLTSSPLSCWR-P 265
 DB ACVAIYVHNPQOMLTHLLTYAEFLGLFLLEMSLKNYKMGPR---LYHSSNCPDFG 546
 QY 266 EMYGLL--SLMDWTRM-----LNNLIVREFLRITPSKPPAAVASTVLGYONKRAFGI 318
 DB VVQGISREYVWAFIRPSTSGISVLRALRLRIKIRKYVASLNLVSSLSMSKSIISL 606
 QY 319 LVVWY---VYFATIGLIFGVIVIALPQNSSLAPANSACGSGFEQLEYANNRPDDPA 375
 DB LFLFLFVIFVAFALGKQIFGRENENDTPSA-----NFDTPPA 646
 QY 376 LVTLMLNLVNNV--QVFLDAYRRY---SGPWSKIYFVLMVSSVYVNLFLALLENF 430
 DB IITVFQILTEGDMNEVYNGIRSGGVSSGWSAIFYITLFLFCNYTLNLFLAIVDNL 706
 QY 431 L-----HKMDPRSHLOPLAGTPPATIOMYELLFRDLEPGEDEL 471
 DB ANAOELTKDEOEDEEAFENOKHALOKAKEVSPSAPNPSIERDRRRHHMSWBRSSH 766
 QY 472 TERLSOH 478
 DB 767 RERRRRH 773
 RESULT 6
 CCAD_MESAU STANDARD; PRT; 1610 AA.
 ID CCAD_MESAU
 AC Q99244; Q99245;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha-1 polypeptide isoform 2).
 GN CACNA1D OR CACNA1A2 OR CCHLA2 OR CACH3 OR CACNA4.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
 NC Mesocricetus.
 NX NCBI_Taxid=10036;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM HCA3A).
 RC TISSUE=Insulinoma;
 RX MEDLINE=93149124; PubMed=1337146;
 RA Yaney G.C., Wheeler M.B., Wei X., Perez-Reyes E., Birnbaumer L.,
 RT Boyd A.E., III, Moss L.G.;
 RT "Cloning of a novel alpha 1-subunit of the voltage-dependent calcium
 RT channel from the beta-cell."
 RL Mol. Endocrinol. 6:2143-2152(1992).
 RN [2]
 RP SEQUENCE OF 1146-1441 FROM N.A. (ISOFORMS CAC3B AND CAC3D).
 RC TISSUE=Heart;
 RX MEDLINE=91056091; PubMed=2173707;
 RA Perez-Reyes E., Wei X., Castellano A., Birnbaumer L.;
 RT "Molecular diversity of L-type calcium channels. Evidence for
 RT alternative splicing of the transcripts of three non-allelic genes."
 RL J. Biol. Chem. 265:20430-20436(1990).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-ID
 CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
 CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
 CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
 CC PHENYLALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-IIIA
 CC (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
 CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FOR-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; HCA3A (SHOWN HERE),
 CC CAC3B AND CAC3D; ARE PRODUCED BY ALTERNATIVE SPLICING. CAC3B
 CC IS IDENTICAL TO HCA3A IN THE FRAGMENT SEQUENCED.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART AND SKELETAL MUSCLE.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; M57969; AAB59702.1; -;
 DR EMBL; M57970; AAB62807.1; -;
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing.
 FT REPEAT 112 408 I.
 FT REPEAT 508 754 II.
 FT REPEAT 871 1153 III.
 FT REPEAT 1190 1465 IV.
 FT DOMAIN 1 125 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 126 144 S1 OF REPEAT I (POTENTIAL).

FT	DOMAIN	145	162	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	163	182	S2 OF REPEAT I (POTENTIAL).
FT	DOMAIN	183	194	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	195	213	S3 OF REPEAT I (POTENTIAL).
FT	DOMAIN	214	234	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	235	253	S4 OF REPEAT I (POTENTIAL).
FT	DOMAIN	254	272	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	273	292	S5 OF REPEAT I (POTENTIAL).
FT	DOMAIN	293	380	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	381	405	S6 OF REPEAT I (POTENTIAL).
FT	DOMAIN	406	522	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	523	542	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	543	557	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	558	576	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	577	584	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	585	603	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	604	613	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	614	632	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	633	651	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	652	672	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	673	726	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	727	751	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	752	884	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	885	903	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	904	919	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	920	939	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	940	951	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	952	970	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	971	976	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	977	996	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	997	1015	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1016	1035	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1036	1125	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1126	1146	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1147	1203	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1204	1222	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1223	1237	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1238	1257	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1258	1264	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1265	1286	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1287	1311	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1312	1331	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1332	1350	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1351	1370	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1371	1437	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1438	1462	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1463	1610	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1	6	POLY-MET.
FT	DOMAIN	652	658	POLY-LEU.
FT	TRANSMEM	826	836	POLY-GLU.
FT	DOMAIN	428	445	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	363	363	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	704	704	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1099	1099	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1404	1404	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	BINDING	1073	1163	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1418	1484	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1430	1473	TO PHENYLALKYLAMINES (BY SIMILARITY).
FT	MOD_RES	1473	1473	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1491	1502	POTENTIAL.
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	224	224	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1261	1303	GFSSDAMNPFSLIYGSIIIVASLSEADPSESILPFPAT PG->HYFTDAMNPFSLIYGSVVDIAITFEVN (IN ISOFORM CAC3D).
FT	SEQUENCE	1610 AA;	182327 MM;	B3B2E3794D936F79 CRC64;


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FT TRANSMEM 1464 1483 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1484 1491 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1492 1510 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1511 1519 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1520 1538 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1539 1557 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1558 1577 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1578 1638 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1639 1663 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1664 2223 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 40 POLY-ALA.
FT DOMAIN 729 735 POLY-GLU.
FT DOMAIN 1064 1068 POLY-SER.
FT DOMAIN 386 403 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT SITE 321 321 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 671 671 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1323 1323 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1611 1611 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT CA_BIND 439 450 BY SIMILARITY.
FT MOD_RES 1674 1674 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CA_BIND 1692 1703 BY SIMILARITY.
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1300 1300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1519 1519 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2223 AA: 251827 MW: 59722DC03E1CFC5B CRC64:

Query Match 7.28; Score 189.5; DB 1: Length 2223;
Best Local Similarity 19.98; Pred. No. 6.2e-07;
Matches 107; Conservative 87; Mismatches 197; Indels 147; Gaps 25;

QY 43 CRFGSGDDGQDRKITYFQNLPESLGLVLTPANNPDVITPKSNRRAVA-----IF 97
DB 291 CSYWGIPNDG-----ITQFDNLFALLVFOCITMEGWTTLI--YNTDDALGAMNMNLY 342
QY 98 FIVEFVIGSLFLMNLITLITISQF-----RGYLMKSLQTSIFRRRLGTRA-----A 143
DB 343 FIPILITISFVNLVYLGVSFGEFAKEREVENRNSFLKLRQOOIEBELNGYRAMIDKA 402
QY 144 FEVL---SSWVGEGGAPQATRRG--DSTSLRFGCRAPSSSATTTTLTWTGSSP----- 192
DB 403 EEVMLEENKKNAGEKSAI-HYLRRATIKKRMEMIQTESSEDOYTEISSVG--SPLARAS 459
QY 193 -----W-----OTWCFPACGW---CMQO 207
DB 460 IKSTKLEGGSYFRKKERMLRISIRHMKSHAFTYIVLGLVALNTVCVAVHYDQPLMLS 519
QY 208 MCCLISVMTSSMGFSTASSLCTTCWCSCSRSLPMACEGTCPTPATCLIGSSPLSCWR--PE 266
DB 520 NPLVYAEFTFLGTPS--SEMFLKMYGCGPR-----LTFHSSFNFDGCV 561
QY 267 MVGLL--SLMDTRM-----LMLIVFRFLRITSPKMPMAVAVSTVLGLVQNMRAFGTL 319
DB 562 IIGSFIDFVWYTIIREPTEFGISVFLALRLIRFKITKRWASIRNLVYLSMSKMSITSL 621
QY 320 VVVV---VVFALIGINIFRGYIVALLPGNSILAPANGSAPCGSEFDELEVANNPDFPAAL 376
DB 622 FLULFLFIYVFDLGLQGLGG-----QNFEEGTGP-----TNEDEFPAAI 661
QY 377 VTLNMLAVNNM--QVFLDAYRRY---SGPMKIFIVLMMLVSSVIVNLFALILEFLL 431
DB 662 ITVFQILGEGDMNEVMYNGIKSGGVNSGMSSVYFIVLTFGNTLLFLAIVADNIA 721
QY 432 HKMPDRSLQPLAGTPPEATYQVVELLRDI--LEEPGEDELTERLSQHPH--LWLCR 485
DB 722 NAOELTKEEQ---EEEAINKHALOKAKEVSPMSAPGFPSTERRRHKHMSIWEAR 776

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CCAF_HUMAN
ID CCAF_HUMAN STANDARD: PRT: 1966 AA.
AC 060840; 043901;
DT 15-0UL-1999 (Rel. 38, created)
DT 15-0UL-1999 (Rel. 38, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1f subunit.
GN CACNA1F OR CACNA1F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS CSN2 D-369; Q-508; W-1049 AND
RP H-1364.
RC TISSUE=Retina.
RX MEDLINE=98324776; PubMed=9662399;
RA Strom T.M., Nyakatura G., Apfelstedt-Sylla E., Hellebrand H.,
RA Lorenz B., Weber B.H.F., Wutz K., Gutwillingner N., Ruether K.,
RA Drescher B., Sauer C., Zrenner E., Meitinger T., Rosenthal A.,
RA Meindl A.;
RT "An L-type calcium channel gene mutated in incomplete X-linked
RT congenital stationary night blindness.";
RL Nat. Genet. 19:260-263(1998).
[2]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U.,
RA Meindl A., Rosenthal A.; the EMBL/Genbank/DBJ databases.
RL Submitted (Feb-2000) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE OF 1200-1966 FROM N.A.
RX MEDLINE=9808923; PubMed=9344658;
RA Fisher S.E., Ciccodicola A., Tanaka K., Curci A., Desicato S.,
RA D'Urso M., Craig I.W.;
RT "Sequence-based exon prediction around the synaptophysin locus reveals
RT a gene-rich area containing novel genes in human proximal Xp.";
RL Genomics 45:340-347(1997).
-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP).
CC PHENYLTALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-IIIA
CC (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSION IN SKELETAL MUSCLE AND RETINA.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- DISEASE: DEFECTS IN CACNA1F ARE THE CAUSE OF INCOMPLETE X-LINKED
CC CONGENITAL STATIONARY NIGHT BLINDNESS (CSN2), A NONPROGRESSIVE
CC RETINAL DISORDER CHARACTERIZED BY DECREASED VISUAL ACUITY AND LOSS
CC OF NIGHT VISION.
-1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
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CC the European Bioinformatics Institute. There are no restrictions on its
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DR EMBL: AJ006216; CAA06916.1; -
 DR EMBL: AJ224874; CAA12175.1; -
 DR EMBL: AF235097; AAF62518.1; -
 DR EMBL: U93305; AAB92359.1; -
 DR MIM: 300110; -
 DR MIM: 300071; -
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans; 4.
 DR PRINTS: PRO0167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Disease mutation; Vision.

FT REPEAT 79 375 I.
 FT REPEAT 504 750 II.
 FT REPEAT 847 1129 III.
 FT REPEAT 1166 1433 IV.
 FT DOMAIN 1 92 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 93 111 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 112 129 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 130 149 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 150 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 180 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 181 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 220 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 221 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 259 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 260 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 372 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 373 518 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 519 538 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 539 553 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 554 572 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 573 580 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 581 599 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 600 609 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 610 628 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 629 647 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 648 668 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 669 722 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 723 747 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 748 860 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 861 879 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 880 895 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 896 915 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 916 927 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 928 946 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 947 952 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 953 972 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 973 991 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 992 1011 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1012 1101 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1102 1122 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1123 1179 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1180 1198 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1199 1213 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1214 1233 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1234 1240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1241 1262 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1263 1279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1280 1299 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1300 1318 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1319 1338 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1339 1405 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1406 1430 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1431 1966 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 648 654 POLY-LEU.

FT DOMAIN 783 788 POLY-GLU.
 FT DOMAIN 798 814 POLY-GLU.
 FT DOMAIN 1110 1113 POLY-ILE.
 FT DOMAIN 1629 1634 POLY-GLU.
 FT DOMAIN 395 412 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
 FT SITE 330 330 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 700 700 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1075 1075 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1372 1372 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT BINDING 1049 1139 TO DIHYDROPYRIDINES (BY SIMILARITY).
 FT BINDING 1386 1452 TO DIHYDROPYRIDINES (BY SIMILARITY).
 FT BINDING 1398 1441 TO PHENYLALKYLAMINES (BY SIMILARITY).
 FT MOD_RES 1441 1441 PHOSPHORYLATION (BY CARK) (POTENTIAL).
 FT CA_BIND 1459 1470 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 295 295 G->D (IN CSNB2).
 FT VARIANT 369 369 /FTid-VAR.001504.
 FT VARIANT 508 508 R->Q (IN CSNB2).
 FT VARIANT 508 508 /FTid-VAR.001505.
 FT VARIANT 1049 1049 R->W (IN CSNB2).
 FT VARIANT 1049 1049 /FTid-VAR.001506.
 FT VARIANT 1364 1364 L->H (IN CSNB2).
 FT CONFLICT 1225 1225 E->V (IN REF. 3).
 FT CONFLICT 1265 1271 MISSING (IN REF. 3).
 FT CONFLICT 1652 1767 MISSING (IN REF. 3).
 FT CONFLICT 1849 1849 A->G (IN REF. 3).
 SO SEQUENCE 1966 AA; 219494 MW; FEB47B19FA57E31D CRC64;

Query Match 7.1%; Score 187.5; DB 1; Length 1966;
 Best Local Similarity 18.6%; Pred. No 7.8e-07;
 Matches 101; Conservative 73; Mismatches 169; Indels 199; Gaps 20;

OY 4 ACWEATGRCRLGGGMMVPTGVRGLELSLWGGDPVFWSCFCSQDDGDRRLTYFQN 63
 DB 291 ACTLNGTCR--GRMPGNGGI-----TFNDN 315
 OY 64 LPESLTSLLVLTTRANNDDVMIPAYSKRRA-----IFTVVIGSIFLMLTLTIY 118
 DB 316 FFFAALTVFCVTEGWTDVL--YMDAMGYELPWYFVSLVFFSFLVNLVLGVLS 372
 OY 119 SQF-----RGYLNKSLQ-----TSL 133
 DB 373 GEFSEKREKAKARGDFOKREKQOMEDLRGYLDWITQAEELDMEDSADNGLPOLAEL 432
 OY 134 FRRRLG-----TRAAEVLS-----SMV-----GEGAPQATR----- 162
 DB 433 TNRRRGRLRWFESHSTSHSTSHASLSPASDTGSMTEGDEDEGALASCTRLKIM 492
 OY 163 -----RGSTSLRF--CRAPSSSA-----TTTTLTGTSPPQWCPFCASV 203
 DB 493 KTRCRLRRANRVARRACRAVKSACWYAVLLVFLNLTITLASEHIGQFWLTQIOEX 552
 OY 204 CWMQCCLLSY--MTSSWGFSTASSLCT-----TCWSCCSRLPWACEGTCTPATATG 256
 DB 553 ANKVTLICFLYEMLLKXGLGSPAYVSSFFNRFCFVVC-----GILETIVEVGA 604
 OY 257 SSPLSCWRPEWVGLISLWDMTLMMLIVERELRIIDSKPMVAVASTVGLVONMRAFG 316
 DB 605 MQPLG-----ISVLRCVLLRIFFVTRHMASLSMLVASILNMSKSLA 646
 OY 317 GLIVVY---YFALIGINIFRGVIVALLPGNSSLAPANGSAPCSFQOLEYMANNPDEFA 373
 DB 647 SLTLLEFLFIIFISLGLQFEGKF-----NFDQTHRKSTFTEP 687
 OY 374 AALVTLMNLVNNMVOVL--DAYRRYSQPMK-----YFVLMVLSSVIVNLFALITL 427
 DB 688 QALIVFQILGDMNVMYMDIGMAYGGPFPPGMLVCILYFIILFCNGNITLILNVLAIIV 747

QY 428 EN 429
Db 748 DN 749

RESULT 9
CCAD_HUMAN
ID CCAD_HUMAN STANDARD; PRT; 2161 AA.
AC 001668; Q13916; Q13931;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 2).
GN CACNA1D OR CACNA1A2 OR CCHLA2 OR CACH3 OR CACNA4.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (NEURONAL-TYPE ISOFORM).
RC TISSUE-Neuroblastoma;
RX MEDLINE-92110010; PubMed-1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelcbl G., Ellis S.B., Harpold M.M.;
RT Structure and functional expression of alpha1, alpha2, and beta subunits of a novel human neuronal calcium channel subtype.";
RL Neuron 8:71-84(1992).
RN [2]
RP SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM).
RC TISSUE-Pancreatic islets;
RX MEDLINE-92115705; PubMed-130948;
RA Seino S., Chen L., Seino M., Blondel O., Takeda J., Johnson J.H., Bell G.I.;
RT "Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expressed in pancreatic beta cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:584-588(1992).
RN [3]
RP SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM), AND VARIANT NIDDM.
RX MEDLINE-96044438; PubMed-7557998;
RA Yamada Y., Masuda K., Li Q., Ihara Y., Kubota A., Mura T., Nakamura K., Fujii Y., Seino S., Seino Y.;
RT "The structures of the human calcium channel alpha 1 subunit (CACNA1A2) and beta subunit (CACNB3) genes.";
RL Genomics 27:312-319(1995).
RN [4]
RP FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYALKALAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-III (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
RN [5]
RP SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
RN [6]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [7]
RP ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; NEURONAL-TYPE (SHOWN HERE) AND BETA-CELL-TYPE, ARE PRODUCED BY ALTERNATIVE SPLICING.
RN [8]
RP TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN, WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.
RN [9]
RP DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS

CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT ARG TRINUCLEOTIDE
CC REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS
CC BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES
CC MELLITUS (NIDDM).
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
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CC EMBL; D44085; BAA07804.1; JOINED.
CC EMBL; D44086; BAA07804.1; JOINED.
CC EMBL; D44087; BAA07804.1; JOINED.
CC EMBL; D44088; BAA07804.1; JOINED.
CC EMBL; D44089; BAA07804.1; JOINED.
CC EMBL; D44090; BAA07804.1; JOINED.
CC EMBL; D44091; BAA07804.1; JOINED.
CC EMB

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FT REPEAT 113 409 I.
FT REPEAT 509 755 II.
FT REPEAT 873 1155 III.
FT REPEAT 1192 1467 IV.
FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 127 145 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 164 183 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 164 195 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 196 214 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 215 235 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 236 254 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 255 273 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 274 293 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 294 381 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 382 406 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 407 523 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 524 543 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 544 558 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 559 577 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 578 585 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 586 604 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 605 614 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 615 633 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 634 652 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 653 673 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 674 727 S6 OF REPEAT II (POTENTIAL).
FT TRANSSEM 728 752 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 753 866 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 867 905 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 906 921 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 922 941 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 942 953 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 954 972 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 973 978 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 979 998 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 999 1017 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1018 1037 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1038 1127 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1128 1148 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1149 1205 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1206 1224 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1225 1239 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1240 1259 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1260 1266 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1267 1288 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1289 1313 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1314 1333 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1334 1352 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1353 1372 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1373 1439 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1440 1464 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1465 2161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1 7 POLY-MET.
FT DOMAIN 653 659 POLY-LEU.
FT TRANSSEM 827 838 POLY-GLU.
FT DOMAIN 429 446 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT SITE 364 364 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 705 705 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

```

Query Match 7.1%; Score 187; DB 1; Length 2161;
 Best Local Similarity 18.5%; Pred. No. 9.4e-07;
 Matches 94; Conservative 81; Mismatches 157; Indels 176; Gaps 20;

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OY 12 CRLLGGMMVPIGWYRGLESLMGSDPVVWMSCRCSQDDGQDREKRTIYQNLPELSLSL 71
DB 333 CR--SGWVGNGI-----TNDNFAFALTV 357
OY 72 LVLLTANPVMIPVSKNRVAV-----IPFIVFVIGSLFLNLLTALITYSOFKSYLM 126

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DB 358 FOCITMEGWTDVL---YWMNDAMGFELPNVYFVSLVIFGSPFVLNLVLGLVSGEFSKERE 414
OY 127 KSLQTSLEFRRRLGTRAFEVYLSMVG-----EGG-----APF----- 158
DB 415 KAKRGDQKREKQQLBEDLKGVLDTQAEIDIDPNEEGEGEGRKNTSMPTSESY 474
OY 159 -----QATRGSTSLRRCRAPSSSATTTLTWTGSSPWOTWCF-----AC 201
DB 475 NFEVSGEGENRGCGSL--QALSKSK-----LSRRWRMNFNRRCRAAVKSV 523
OY 202 SWCMWMOCL-LSVMTSS-----WGF-----STASSLCTTQNSC-----GSRSLP--- 240
DB 524 TFYMLVYLVPLVNLTLISSEHYNPDMLTQIODIANVLLALFCEMLVKMYSIGLOAYF 563
OY 241 -----WACGTCTPATCTLGSSPLSCWBPENYGLLSLMDTRMLMLVFERFLR 290
DB 564 VSLRFRCFCFVCGGITETLIVELIMSPLG-----ISVFCVALLR 625
OY 291 IIPSKRPAAVVAASYLVQNMRAFGILVYV---YVFAIIGINLFRVYVALPGNSL 347
DB 626 IFKVTFRHTSLCNLVASILNSKSSASILLFLFIIIFSLGMLGGRF----- 676
OY 348 APANSAACGSEFQLEYMANNFDEFAALVTLMLLVNNMWQ-VFLDAYRRYSGPMGK-- 404
DB 677 -----NDEFOYTKRSTFDNFPQALLVFOILGEDMNAVYDGMAYGGPSSSGM 726
OY 405 ---IFVLMVLVSSVYVNLFLALLEN 429
DB 727 IVCIVFIILFCIGNTILNLVFLAYAVDN 754

RESULT 10
ID CAE_RABIT STANDARD; PRT; 2259 AA.
AC 002343; 002344;
DB 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
BT Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (Brain calcium channel II) (BII).
DE CACNA1E OR CACNA1A6 OR CACNA6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92354772; PubMed=1379552;
RA Nidome T., Kim M.S., Friedrich T., Mori Y.;
RT "Molecular cloning and characterization of a novel calcium channel from rabbit brain.";
RL FEBS Lett. 308:7-13(1992).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-ACATOXIN-IIA (OMEGA-AGA-IIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA

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CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BII-1 (SHOWN HERE) AND BII-2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE CEREBRAL CORTEX, HIPPOCAMPUS,
 CC AND CORPUS STRIATUM.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X67855; CAA48040.1; -;
 DR EMBL: X67856; CAA48041.1; -;
 DR PIR: S29236; S29236.
 DR PIR: S29237; S29237.
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Cat_channel_Tryp.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans; 4.
 DR PRINTS: PR00167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing.
 FT REPEAT 76 354 I.
 FT REPEAT 76 706 II.
 FT REPEAT 1130 1414 III.
 FT REPEAT 1453 1716 IV.
 FT DOMAIN 1 89 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 90 108 S1 OF REPEAT I.
 FT DOMAIN 109 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 146 S2 OF REPEAT I.
 FT DOMAIN 147 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 176 S3 OF REPEAT I.
 FT DOMAIN 177 185 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 186 204 S4 OF REPEAT I.
 FT DOMAIN 205 223 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 224 243 S5 OF REPEAT I.
 FT DOMAIN 244 326 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 327 351 S6 OF REPEAT I.
 FT DOMAIN 352 476 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 477 495 S1 OF REPEAT II.
 FT DOMAIN 496 510 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 511 530 S2 OF REPEAT II.
 FT DOMAIN 531 538 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 539 557 S3 OF REPEAT II.
 FT DOMAIN 558 567 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 567 586 S4 OF REPEAT II.
 FT DOMAIN 587 605 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 606 625 S5 OF REPEAT II.
 FT DOMAIN 626 678 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 679 703 S6 OF REPEAT II.
 FT DOMAIN 704 1143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1144 1162 S1 OF REPEAT III.
 FT DOMAIN 1163 1178 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1179 1198 S2 OF REPEAT III.
 FT DOMAIN 1199 1210 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1211 1229 S3 OF REPEAT III.
 FT DOMAIN 1230 1243 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1244 1262 S4 OF REPEAT III.
 FT DOMAIN 1263 1281 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1282 1301 S5 OF REPEAT III.

FT DOMAIN 1302 1388 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1389 1413 S6 OF REPEAT III.
 FT DOMAIN 1414 1468 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1469 1487 S1 OF REPEAT IV.
 FT DOMAIN 1488 1502 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1503 1522 S2 OF REPEAT IV.
 FT DOMAIN 1523 1530 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1531 1549 S3 OF REPEAT IV.
 FT DOMAIN 1550 1561 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1562 1580 S4 OF REPEAT IV.
 FT DOMAIN 1581 1599 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1600 1619 S5 OF REPEAT IV.
 FT DOMAIN 1620 1688 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1689 1712 S6 OF REPEAT IV.
 FT DOMAIN 1713 2259 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1716 721 POLY-GLU.
 FT DOMAIN 748 753 POLY-ARG.
 FT TRANSMEM 767 772 POLY-ARG.
 FT DOMAIN 1218 1221 POLY-VAL.
 FT TRANSMEM 1976 1979 POLY-SER.
 FT DOMAIN 2231 2235 POLY-ARG.
 FT TRANSMEM 374 391 BINDING TO THE BETA SUBUNIT (BY
 FT SIMILARITY).
 FT SITE 309 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 657 (BY SIMILARITY).
 FT SITE 657 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 1362 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 1362 (BY SIMILARITY).
 FT SITE 1653 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 1653 (BY SIMILARITY).
 FT CA_BIND 426 437 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 1724 1724 BY SIMILARITY.
 FT CA_BIND 1742 1753 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1556 1556 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1561 1561 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 2101 2259 HSRLDLPVPRPLSYSLKQSPNSPSPADSGSL
 FT LSPALPSNOVGLPSSDPSRAQGSHPQVISEPYAL
 FT HEDSHASDGEETLTLEAAVATSLGRSTTISAPRLRSM
 FT QMPNGHYRRRRGPGAGLCAVAGDLSDEDC -> Q
 FT QMPQEEVGLPHQCGPCDRMRMPGRMSGKSHSP
 FT LPHGCRDSTGAGAGPPRCYSGAGADAGTCDLSLP (IN
 FT ISOFORM BII-2).
 SQ SEQUENCE 2259 AA; 254250 MW; E4A75707638779E CRC64;
 Query Match 7.1%; Score 187; DB 1; Length 2259;
 Best Local Similarity 18.1%; Pred. No. 9; 9e-07;
 Matches 102; Conservative 91; Mismatches 207; Indels 162; Gaps 18;
 QY 32 LMGDPVYVWMSQRFSGQDGDGD---RRLTYFQNLPSLSLVLTLTANNPDVMDA 87
 DB 259 LRGFDPPHPCGVGGCAGTECKDWMIGPNDGITFDNLTFAVLTVFOCTIEGTYVL--- 315
 QY 88 YEKNRAYA-----IPFIVTVIGSLIMNLTAIYSQF-----RGYLMKSLQTS 132
 DB 316 YTNMALGATWMTWLYTIPILIIISFEVNLVIGVLSGEFAKERERYENRAFAKLRRQO 375
 QY 133 LRRRLRGTAAREVYSSMYGEGGAPQATRRGPSTSLRCRAPSSSATTTTLTWGTSSTP 192
 DB 376 IERELNGYRAMDKAEVW-----LAENKNGSTALEVLRATIKRSRTTEAMTRDSSD- 429
 QY 193 WGTWCPFACSWCMQMCCLSVWTS-----EHCYVSISSVGTPLAASIKSAVDASVFRKRELLRISVRAVVS 475
 DB 430 -----EHCYVSISSVGTPLAASIKSAVDASVFRKRELLRISVRAVVS 475
 QY 219 ---WGFSTASSLCTTWCSCCSRLP-WACE-----GTCPTPA 251
 DB 476 QVFWIVLISLVALNTRCAVAVIHNNQPOWTLHLYVAEFLGLFLEMSLKYGMQPR-- 533
 QY 252 TGLTSSPLSCMR-PEMWGLL--SLMDKTRM-----LNNLTYFRPLRIIPSKPAVAVAS 303
 DB 534 --LYFHSSFNCFDGVTVGSIIEVVAIRPQTSFGISVLRALRLRIKRIKRYASLRN 591


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CC EMBL: X05921; CAA29355.1; -
DR EMBL: M23919; AAA31159.1; -
DR PIR: A30063; A30063; -
DR InterPro: IPR002077; Ca_channel.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR Pfam: PF00520; Ion_trans_4.
DR PRINTS: PR00167; CACHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Polymorphism.
FT REPEAT 38 337
FT REPEAT 418 664
FT REPEAT 786 1068
FT REPEAT 1105 1384
FT DOMAIN 1 51
FT TRANSMEM 52 70
FT TRANSMEM 71 88
FT TRANSMEM 89 108
FT TRANSMEM 109 120
FT TRANSMEM 121 139
FT TRANSMEM 140 160
FT TRANSMEM 161 179
FT TRANSMEM 180 198
FT TRANSMEM 199 218
FT TRANSMEM 219 309
FT TRANSMEM 310 334
FT TRANSMEM 335 342
FT TRANSMEM 433 451
FT TRANSMEM 452 466
FT TRANSMEM 467 486
FT TRANSMEM 487 494
FT TRANSMEM 495 513
FT TRANSMEM 514 523
FT TRANSMEM 524 542
FT TRANSMEM 543 561
FT TRANSMEM 562 581
FT TRANSMEM 582 636
FT TRANSMEM 637 661
FT TRANSMEM 662 799
FT TRANSMEM 800 818
FT TRANSMEM 819 834
FT TRANSMEM 835 854
FT TRANSMEM 855 866
FT TRANSMEM 867 885
FT TRANSMEM 886 892
FT TRANSMEM 893 911
FT TRANSMEM 912 930
FT TRANSMEM 931 950
FT TRANSMEM 951 1040
FT TRANSMEM 1041 1065
FT TRANSMEM 1066 1118
FT TRANSMEM 1119 1137
FT TRANSMEM 1138 1152
FT TRANSMEM 1153 1172
FT TRANSMEM 1173 1180
FT TRANSMEM 1181 1199
FT TRANSMEM 1200 1231
FT TRANSMEM 1232 1250
FT TRANSMEM 1251 1269
FT TRANSMEM 1270 1289
FT TRANSMEM 1290 1356
FT TRANSMEM 1357 1381
FT TRANSMEM 1382 1873
FT TRANSMEM 1383 374
FT TRANSMEM 357 568
FT TRANSMEM 562 292
FT SITE 292
FT SITE 614
FT SITE 614
FT SITE 1014
FT SITE 1014

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FT (BY SIMILARITY).
Query Match 7.1%; Score 186; DB 1; Length 1873;
Best Local Similarity 18.1%; Pred. No. 9,7e-07;
Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;

QY 58 LTVFQNLPELSLILVLTANNPDVMI PAVSKRAYA-----IEFVTVYIGSLFLML 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 272 ITHFDNFGFSLVYQGITMGMTDVL---YVNDALGNEMPIYFVTLILGSEFFIINTL 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 LTAITYQFQGYLMLKSLQTSIFRRRLGTRAFVYLSMVG----- 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 VLGLSEFTRKEREKASRGTFQRLREKQOLEEDREGVMSWITGGEVYDLEKGLSL 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 -EGGAFPOATR--RGFSTSLFCRAPASSSATTLTWTGTSPPQWT---CPFACS--- 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 EGGSDTESLEYELGKLKTIQFIR-----HWRQNNRYFRMKCHLYK 430
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 ---WCMQMC-----CLLSVMT-----SSWGFSTAS 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 431 SRVFWVLVILVALNTLSIASEHNQPLMLTHQDIANRVLSFTLEMLKMYGLGRQ 490
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 226 SLCT-----TCWSCSSSLP-WACEGICPPATCLTGSSPLSCRPPEVGLSLMDTRM 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 YFMSIFNRFDYFVCSGILELLEVESGAMP---LGISVLR----- 529
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 280 LNMILVFRFLRIIPMKPMAYVASTVGLVQNMRAFGLIIVVY---YFAIIGINLFRG 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 530 -----IRLRLFKITKWTSLNVLVSLNLSIASLILLLFLFIIFALDMQLFG 583
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 VIVALPQNSLAPANGAPCGSPQLEWMANFDFAALVTLNMLVYNNM-OVFLDAY 395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 584 RY-----DFEDTEVRNSNPNFQALISVFOVLGEQMNVMYNGI 624
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 396 RRYGPMK-----IYVLMVLVSVIVNLFALILENLFH-----KMDPRSHL 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 625 MAYGSPGVGLVYCIYFIIFVCGNYTLINVLVLAIVDNLEASLSAQAKAEKRRR 684
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 441 QPLAGTEPATVQMTVELLFRDILEPGEDELTERLSQHP 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 685 KMSRGLPKT-----EERKSVAKKLEQKP 709
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
CCAS_HUMAN STANDARD; PRT; 1873 AA.
AC Q13696; Q13934; Q12896;
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1s subunit (Calcium
DE channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle).
GN CACNL1A3 OR CACNL1A3 OR CACNL1A3 OR CACNL1A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95229168; PubMed=7713519;
RA Hogan K., Powers P.A., Gregg R.G.;
RT "Cloning of the human skeletal muscle alpha 1 subunit of the
RT dihydropyridine-sensitive L-type calcium channel (CACNL1A3).";
RL Genomics 24:608-609(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96435439; PubMed=8838325;
RA Hogan K., Gregg R.G., Powers P.A.;
RT "The structure of the gene encoding the human skeletal muscle alpha 1
RT subunit of the dihydropyridine-sensitive L-type calcium channel
RT (CACNL1A3).";
RL Genomics 31:392-394(1996).

```


[3] SEQUENCE OF 1200-1300 FROM N.A., AND VARIANTS HYPOKPP GLY-1239 AND HIS-1239.
 MEDLINE-94273190; PubMed-8004673;
 RA Placsek L.J., Tawil R., Griggs R.C., Engel A.G., Layzer R.B.,
 RA Kielesni H., McManis P.G., Santiago L., Moore M., Fouad G.,
 RA Bradley F., Leppert M.F.;
 RT "dihydropyridine receptor mutations cause hypokalemic periodic
 RT paralysis.";
 RT Cell 77:863-868(1994).
 RN [4]
 RP SEQUENCE OF 1223-1413 FROM N.A.
 RA Soldatov N.M.;
 RT "human skeletal muscle L-type Ca2+ channel alpha 1S subunit gene shows
 RT splitting patterns similar to alpha 1C and alpha 1D genes in the region
 RT involved in hereditary disorders.";
 RT Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 788-830: 1019-1085 AND 1293-1318 FROM N.A.
 RX MEDLINE-93162636; PubMed-7916735;
 RA Gregg R.G., Couch F., Hogan K., Powers P.A.;
 RT "Assignment of the human gene for the alpha-1 subunit of the skeletal
 RT muscle DHP-sensitive calcium channel (CACNL1A3) to chromosome 1q31-
 RT q32.";
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 RP VARIANT HYPOKPP HIS-528.
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 RA Jurkat-Rott K., Lehmann-Horn F., Elbaz A., Heine R., Gregg R.G.,
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 RA Monnier N., Procaccio V., Stieglitz P., Lunardi J.;
 RT "Malignant-hyperthermia susceptibility is associated with a mutation
 RT of the alpha-1-subunit of the human dihydropyridine-sensitive L-type
 RT voltage-dependent calcium-channel receptor in skeletal muscle.";
 RT Am. J. Hum. Genet. 60:1316-1325(1997).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S
 CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
 CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
 CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
 CC PHENYLALETAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-111A
 CC (OMEGA-AGA-111A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
 CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT
 CC ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN
 CC ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
 CC CHANNEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S4, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE
 CC RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE
 CC FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.

CC -1- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL
 CC FUNCTION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN CACNL1A3 ARE THE CAUSE OF HYPOKALEMIC PERIODIC
 CC PARALYSIS (HYPOKPP OR HOKPP1), AN AUTOSOMAL DOMINANT SKELETAL
 CC MUSCLE DISORDER MANIFESTED BY EPISODIC WEAKNESS ASSOCIATED WITH
 CC LOW SERUM POTASSIUM. MUSCLE WEAKNESS COULD BE DUE TO ALTERED
 CC EXCITATION-CONTRACTION COUPLING IN HYPOKPP PATIENTS.
 CC -1- DISEASE: DEFECTS IN CACNL1A3 ARE THE CAUSE OF MALIGNANT
 CC HYPERTHERMIA SUSCEPTIBILITY 5 (MHSS); AN AUTOSOMAL DOMINANT
 CC DISORDER THAT IS POTENTIALLY LETHAL IN SUSCEPTIBLE INDIVIDUALS ON
 CC EXPOSURE TO COMMONLY USED INHALATIONAL ANESTHETICS AND
 CC DEPOLARIZING MUSCLE RELAXANTS.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
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 DR EMBL: U31008; AAB3723

DR MIM: 114208; -
 DR MIM: 170400; -
 DR MIM: 601887; -
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Ca_channel_TrpL.
 DR InterPro: IPR000636; Cation_chan_non_119.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans_4.
 DR PRINTS: PR00167; CACHANNEL.
 KM Ionic channel: Transmembrane.
 KM Calcium channel: Glycoprotein; Repeat; Multigene family;
 FT Calcium-binding; Phosphorylation; Disease mutation; Polymorphism.
 FT REPEAT 38 337 I.
 FT REPEAT 418 664 II.
 FT REPEAT 786 1068 III.
 FT REPEAT 1105 1384 IV.
 FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 52 70 S1 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 71 88 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 89 108 S2 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 109 120 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 121 139 S3 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 140 160 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 161 179 S4 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 180 198 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 199 218 S5 OF REPEAT 1 (POTENTIAL).

Query Match Best Local Similarity 7.0%; Score 184; DB 1; Length 1873;
 Matches 95; Conservative 82; Mismatches 171; Indels 164; Gaps 19;

OY 58 LTFYONLPESLTLVLTANNPDVIMPAYSKNRAVA-----IPFIVTVIGSLFIMNL 112
 DB 272 ITHFNFGSMITVYCTIMEGMTDVL---YWNDAIGNEMPMYVITLILGSEFTLNL 328
 OY 113 LFAIISQFRCGLMKSLSQTSFRRRLGTRAFEVLSMWG----- 152
 DB 329 VLGVLSGETTKERERAKSGTFOKLEKQDDEDLRGVSMITGCEHMDVEDEFREGKLSL 388
 OY 153 EGGAFFQATRR--GPSTSLRCPRAPSSSATTTLTWTGSSPMQWQ---CPFACS---- 202
 DB 389 DEGSDTESLYELINKIQTPIR-----HWKQNRIFRWKCHDIYK 430
 OY 203 -----WCMQMCCLLSVMTSS-----W-----GFSTASLSCTT----- 230
 DB 431 SKVFYWLIVLLVLTLSIASEHNQPLMLTRLODIANRVLLSFTTEKLMKMYGLGRQ 490
 OY 231 -----CMSCCSRSLP--WACGCTPTPATCUTLGSSPLSCWREPMVGLSLMDMTRM 279
 DB 491 YFMSIFNRPDCVFCVSGILELILVESGAMTP---LGISVLNC----- 529
 OY 280 LMLIVFRLRIIPMKPMVAVASTVLGIYONMRAFGGLVVVY---YVFATIGINLFRG 336
 DB 530 -----ILRLRFKTKTKWTSLNIVASLINSIRIASILLFLFYFALGQMLEGG 583
 OY 337 VIVALPGNSSIAPANGAPCGSEFQLEYWANNEDDPAALVTLMLIMLVNNN--QVFLDAY 395
 DB 584 RY-----DFFETEVRSNFDNFQALLISVFOVLGETDTSMMYNGI 624
 OY 396 RRYSGPMWK-----TYFVLMVLVSSVIVNLFALILLENFLHKMPRSLQPLAGTPEAT 450
 DB 635 MAYGSPSPGMLVCTYFTITLFCGNYILLNVLATAVDNL-----AEASLTSQAKK 677
 OY 451 YQMTVELLFRDLEEGDE--LTERLSQHP 479
 DB 678 AEKKRRKMSKGLPKDSEKSTMAKKLEQKP 709

RESULT 13
 CCAC_HUMAN STANDARD; PRT: 2221 AA.
 AC Q13936; Q09025; Q13917; Q13922; Q13919; Q13920; Q13921;
 AC Q13924; Q13925; Q13926; Q13927; Q13928; Q13930; Q13918; Q13929;

AC Q13923; Q13933; Q13932; Q15877; Q99875; Q14744; Q14743;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1c subunit (Calcium
 channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle).
 GN CACNA1C OR CACNL1A1 OR CCHL1A1 OR CAC42 OR CACN2.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM HFCC), AND ALTERNATIVE SPLICING.
 RC TISSUE=Fetal fibroblast.
 RX MEDLINE=92262493; PubMed=1316612;
 RT Soldatov N.M.;
 RT "Molecular diversity of L-type Ca2+ channel transcripts in human
 fibroblasts";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4628-4632(1992).
 [2]
 RP SEQUENCE FROM N.A. (HFCC; NEURONAL ISOFORMS H66-2; H2.05 AND H54).
 RC TISSUE=Lung fibroblast, and Hippocampus;
 RX MEDLINE=95048396; PubMed=7959794;
 RT Soldatov N.M.;
 RT "Genomic structure of human L-type Ca2+ channel";
 RL Genomics 22:77-87(1994).
 [3]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95256214; PubMed=7737988;
 RT Soldatov N.M., Bouron A., Reuter H.;
 RT "Different voltage-dependent inhibition by dihydropyridines of human
 Ca2+ channel splice variants";
 RL J. Biol. Chem. 270:10540-10543(1995).
 [4]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RA Soldatov N.;
 RT "Functional expression of splice variants of human L-type calcium
 channel (isoform 1 gene)";
 RL Submitted (JUN-1994) to the EMBL/Genbank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Hippocampus;
 RX MEDLINE=97166207; PubMed=9013606;
 RA Soldatov N.M., Zuelke R.D., Bouron A., Reuter H.;
 RT "Molecular structures involved in L-type calcium channel
 inactivation";
 RL J. Biol. Chem. 272:3560-3566(1997).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORMS HHT-1; HH05 AND HH06).
 RC TISSUE=Heart;
 RX MEDLINE=93317655; PubMed=8392192;
 RA Schmitz D., Mikala G., Yatani A., Engle D.B., Iles D.E., Segers B.,
 RA Shine R.J., Weighuis D.O., Kloeckner U., Wakamori M., Wang J.-J.,
 RA Melvin D., Varadi G., Schwartz A.;
 RT "Cloning, chromosomal localization, and functional expression of the
 alpha1 subunit of the L-type voltage-dependent calcium channel from
 normal human heart";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6228-6232(1993).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORMS HT-1 AND HT-2), AND ALTERNATIVE SPLICING.
 RC TISSUE=Heart;
 RX MEDLINE=97242615; PubMed=9087614;
 RA Kloeckner U., Mikala G., Eisfeld J., Iles D.E., Strobeck M.,
 RA Mershon J.L., Schwartz A., Varadi G.;
 RT "Properties of three COOH-terminal splice variants of a human cardiac
 L-type Ca2+-channel alpha1-subunit";
 RL Am. J. Physiol. 272:H1372-H1381(1997).
 [8]
 RP SEQUENCE FROM N.A. (ISOFORMS A1C-105 AND A1C-106).
 RA Soldatov N.M.;
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 [9]

RP SEQUENCE OF 1182-1503 FROM N.A. (ISOFORMS CACH2A; CACH2C AND CACH2D).
RC TISSUE-Heart; PubMed=2173707;
RX MEDLINE=91056091; PubMed=2173707;
RA Perez-Reyes E., Wei X., Castellano A., Birnbaumer L.;
RT "Molecular diversity of L-type calcium channels. Evidence for
RT alternative splicing of the transcripts of three non-allelic genes.";
RL J. Biol. Chem. 265:20430-20436(1990).
RN [10]
RP SEQUENCE OF 1140-1206 FROM N.A.
RC TISSUE-Heart;
RX MEDLINE=91363396; PubMed=1653763;
RA Powers P.A., Gregg R.G., Talley P.A., Liao M., Hogan K.;
RT "Assignment of the human gene for the alpha 1 subunit of the cardiac
RT DHP-sensitive Ca2+ channel (CCHL1A1) to chromosome 12p12-pter.";
RL Genomics 10:835-839(1991).
RN [11]
RP SEQUENCE OF 1196-1421 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=93122776; PubMed=1335957;
RA Sun W., McPherson J.D., Hoang D.Q., Wasmuth J.J., Evans G.A.,
RT "Mapping of a human brain voltage-gated calcium channel to human
RT chromosome 12p13-pter.";
RL Genomics 14:1092-1094(1992).
RN [12]
RP MUTAGENESIS AND CALCIUM BINDING.
RX MEDLINE=93293809; PubMed=8099908;
RA Tang S., Mikala G., Bahinski A., Yatan A., Varadi G., Schwartz A.;
RT "Molecular localization of ion selectivity sites within the pore of a
RT human L-type cardiac calcium channel.";
RL J. Biol. Chem. 268:13026-13029(1993).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
CC PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-ACETOXIN-ITIA
CC (OMEGA-AGA-ITIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT
CC ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- ALTERNATIVE PRODUCTS: MULTIPLE ISOFORMS ARE CREATED BY ALTERNATIVE
CC SPLICING EVENTS, WHICH SEEM TO OCCUR IN A TISSUE-SPECIFIC MANNER.
CC ALL THESE SPLICED VARIANTS PROBABLY COMPOSE CHANNELS WITH DIFFERENT
CC GATING PROPERTIES, AND DISPLAY MARKED DIFFERENCES IN THE
CC SENSITIVITY TO DHP COMPOUNDS. THE FIBROBLAST ISOFORM HFCC IS SHOWN
CC HERE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, OVARY, PANCREATIC BETA-
CC CELLS AND IN THE BRAIN.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF
CC INHIBITS THE OPENING OF THE CHANNEL (BY STIMILARITY).
CC -1- PTM: PHOSPHORYLATION BY CAPK ACTIVATES THE CHANNEL (BY
CC STIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
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 Db 611 MSPGISTVRCVRLRIIPKTRRYNSL-----SNLVASILNSVRSIA 652
 QY 317 GILVVVY---YFAIIGINLFRGVIALPGNSLAPANGAPCSFEQLEWANNEDPA 373
 Db 653 SLILLLFLFIIFSLGLQGLGKFE-----NEDMQTRSTEDNFP 693
 QY 374 AALVTLMAMVNMW-QVFLDAYRRYSGPWSK-----IYFVLMVLVSSVWVNFALIL 427
 Db 694 QSLTVEFQILTGEDMNSVMDGIMAYGSPFPMGLVCIFYILFIICNGYIILLNVEFLATAV 753
 QY 428 EN 429
 Db 754 DN 755

RESULT 14
 CCAB_RABIT
 ID CCAB_RABIT STANDARD: PRT: 2339 AA.
 AC 005152;

Dt 15-JUL-1999 (Rel. 38, Created)
 Dt 15-JUL-1999 (Rel. 38, Last sequence update)
 Dt 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Voltage-dependent N-type calcium channel alpha-1B subunit (Calcium channel, L type, alpha-1 polypeptide isoform 5) (Brain calcium channel II) (BIII).
 GN CACNA1B OR CACNA1A5 OR CACNA5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93236885; PubMed=8386525;
 RA Fujita Y., Myllyleht M., Dirksen R.T., Kim M.-S., Nilidome T., Nakai J., Fuhrich T., Iwabe N., Miyata T., Furuichi T., Furutani D., Mikoshiba K., Mori Y., Beam K.G.;
 RT "Primary structure and functional expression of the omega-conotoxin-sensitive N-type calcium channel from rabbit brain.";
 RL Neuron 10:585-598(1993)
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.
 CC -1- HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- PPM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK

CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
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 CC EMBL: D14157; BAA03202.1;
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Cat_channel_Tryp.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans_4.
 DR PRINTS: PRO0167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; ATP-binding.
 FT REPEAT 82 359
 FT REPEAT 469 713
 FT REPEAT 1142 1424
 FT REPEAT 1461 1714
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 FT TRANSMEM 96 114
 FT DOMAIN 115 132
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 FT DOMAIN 1531 1538
 FT TRANSMEM 1539 1557
 FT DOMAIN 1558 1566
 FT TRANSMEM 1567 1585
 FT DOMAIN 1586 1604
 FT TRANSMEM 1605 1624
 FT DOMAIN 1625 1686
 I.
 II.
 III.
 IV.
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).

RL Nature 368:67-70(1994).
 RN [9]
 RP EF-HAND MOTIF AND CALCIUM INACTIVATION.
 RX MEDLINE-96095215; PubMed-7491499.
 RA de Leon M., Wang Y., Jones L., Perez-Reyes E., Wei X., Soong T.W.,
 RA Snutch T.P., Yue D.T.,
 RT "Essential Ca(2+) binding motif for Ca(2+)-sensitive inactivation of
 L-type Ca2+ channels.";
 RL Science 270:1502-1505(1995).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C
 GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
 CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
 GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
 PHENYALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-III
 (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
 GYIA (OMEGA-CTX-GYIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT
 CC ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: At least 4 isoforms; THE HEART ISOFORMS
 CC CAC2A (SHOWN HERE), CAC2C, CAC2D AND A LONG ISOFORM, ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSION IN CARDIAC MUSCLE. IN LUNG,
 CC EXPRESSED IN AIRWAY AND VASCULAR SMOOTH MUSCLE CELLS.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF
 CC INHIBITS THE OPENING OF THE CHANNEL.
 CC -1- PTM: PHOSPHORYLATION BY CAK ACTIVATES THE CHANNEL.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: X15539; CAA33546.1; -
 DR EMBL: X55763; CAA39289.1; -
 DR EMBL: M57974; AAA31182.1; -
 DR EMBL: X60782; CAA43196.1; -
 DR PIR: S05054; S05054.
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR002111; Cal_channel_Tryp.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans; 4.
 DR PRINTS: PR00167; CACHANNL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing.
 FT REPEAT 141 438 I.
 FT REPEAT 540 786 II.
 FT REPEAT 917 1199 III.
 FT REPEAT 1236 1509 IV.
 FT DOMAIN 1 154 CYTOPLASMIC (POTENTIAL).

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
46 CSQDGDGQDERLYFONPESLTVLTNNPDVMIAPSKRARA	18.6%	179.5	DB 1	2171	157	167	Gaps	19
362 CKRGWGC-FKHGTTNDNFAMLTIVFCITMGWTDVL	99; Conservative	86	Mismatches	181	Indels	167	Gaps	19
101 FTVIGSLFMTNLTAITYSQF	100	125						
418 LVFGSFFVNLVGLVSGFSKERRKAKARGDFOLKREKQLEEDLKGLDWTQAEI	477							
126	125							
478 DPENDEGDEKPRMSMPTSETSVNTENAVAGDIEGNCARLAHRISKS	531							
157 FPOATRRGPSTSLRFRASSSSA	203							
532 FSRWRRWNRFPCKRCKRAVKSVMFVYVFLVFLVTLITASHYVQPMWLEVDQTA	590							
204 CMMQCCILSVMTS	256							

Query Match: 6.8%; Score 179.5; DB 1; Length 2171;
 Best Local Similarity: 18.6%; Pred. No. 3.7e-06;
 Matches: 99; Conservative: 86; Mismatches: 181; Indels: 167; Gaps: 19;

FT TRANSMEM 155 173 S1 OF REPEAT I.
 FT DOMAIN 174 190 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 191 211 S2 OF REPEAT I.
 FT DOMAIN 212 223 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 224 242 S3 OF REPEAT I.
 FT DOMAIN 243 262 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 263 281 S4 OF REPEAT I.
 FT DOMAIN 282 300 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 301 320 S5 OF REPEAT I.
 FT DOMAIN 321 410 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 411 435 S6 OF REPEAT I.
 FT DOMAIN 436 554 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 555 573 S1 OF REPEAT II.
 FT DOMAIN 574 588 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 589 608 S2 OF REPEAT II.
 FT DOMAIN 609 616 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 617 635 S3 OF REPEAT II.
 FT DOMAIN 636 645 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 646 664 S4 OF REPEAT II.
 FT DOMAIN 665 683 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 684 703 S5 OF REPEAT II.
 FT DOMAIN 704 758 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 759 783 S6 OF REPEAT II.
 FT DOMAIN 784 930 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 931 949 S1 OF REPEAT III.
 FT DOMAIN 950 965 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 966 985 S2 OF REPEAT III.
 FT DOMAIN 986 997 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 998 1016 S3 OF REPEAT III.
 FT DOMAIN 1017 1023 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1024 1042 S4 OF REPEAT III.
 FT DOMAIN 1043 1061 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1062 1081 S5 OF REPEAT III.
 FT DOMAIN 1082 1171 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1172 1196 S6 OF REPEAT III.
 FT DOMAIN 1197 1249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1250 1268 S1 OF REPEAT IV.
 FT DOMAIN 1269 1283 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1284 1303 S2 OF REPEAT IV.
 FT DOMAIN 1304 1311 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1312 1330 S3 OF REPEAT IV.
 FT DOMAIN 1331 1354 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1355 1373 S4 OF REPEAT IV.
 FT DOMAIN 1374 1392 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1393 1412 S5 OF REPEAT IV.
 FT DOMAIN 1413 1481 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1482 1506 S6 OF REPEAT IV.
 FT DOMAIN 1507 2171 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 458 475 BINDING TO THE BETA SUBUNIT (BY
 FT DOMAIN 684 690 POLY-LEU.

```
Db 591 -----KALLALEFTAEMLKMSISLQOAYVSLFNRPDCT-----VCGSILETIIYETKV 640
QY 257 SSPLSCWREPMVGLSLMDMTMLNLIVRFLRIIPSMKPMAYVASTVLGVQNMRAFG 316
Db 641 MSPLGISVLRVRLRIFKITRWNSL-----SNLVASLNSVRSIA 682
QY 317 GILVVY---YVFAITGINLFRGVIALPGNSSLAPANGSAPCGSFEOLEYMANNPDDFA 373
Db 683 SLILLFLFIIFSLGMOLFSGKF-----NFEDEMOTRRSTFDNFP 723
QY 374 AALVTLMNLVVMNW-QVELDAYRRYSGPMK-----IYFVLWMLVSVIWNLFELAIL 427
Db 724 QSLITVFQIITGEDMNSVMTDGMAYGSPFGMLVCITFIIFTCGNYILNLVFLATAY 783
QY 428 ENFL-----HKWDPRSHLOPLAGTPEATYQMTVELLFRDILEPGEDEL 471
Db 784 DNLADESLTSAQKEEERERKRLART--ASPEKKOEYVGKPALEEAKEEKI 834
```

Search completed: October 8, 2002, 10:03:30
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:10:16 ; Search time 67 seconds
(without alignments)
1252.277 Million cell updates/sec

Title: US-09-918-359-7
Perfect score: 2634
Sequence: 1 MSSACWEATGRCRLGGGMV.....PGEDELTERLSQHPHLWICR 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1180	44.8	371	4 Q9NT82	Q9nt82 homo sapien
2	345	13.1	819	11 Q9NTNS	Q9wtns rattus norv
3	342	13.0	724	10 Q9ZT83	Q9zt83 arabidopsi
4	342	13.0	733	10 Q94KT8	Q94kt8 arabidopsi
5	342	13.0	775	4 Q9ULQ1	Q9ulq1 homo sapien
6	342	13.0	817	11 Q9EJO0	Q9ejoj mus musculu
7	336	12.8	733	10 Q94RT1	Q94rt1 arabidopsi
8	201	7.6	1643	11 Q91WX9	Q91wx9 rattus norv
9	191.5	7.3	2295	11 Q923K6	Q923k6 rattus norv
10	190	7.2	1602	11 Q91W25	Q91w25 mesocricetu
11	189.5	7.2	2125	5 Q96057	Q96057 halocynthia
12	189	7.2	1912	4 Q95226	Q95226 homo sapien
13	189	7.2	1977	4 Q9UH81	Q9uh81 homo sapien
14	189	7.2	2224	4 Q9NYZ6	Q9nyz6 homo sapien
15	186.5	7.1	2162	4 Q9NYZ5	Q9nyz5 homo sapien
16	180.5	6.9	1985	11 Q9JIS7	Q9jis7 mus musculu

17	179.5	6.8	1981	11 Q923Z7	Q923z7 rattus norv
18	177.5	6.7	2331	6 Q9TAA4	Q9tta4 bos taurus
19	175.5	6.7	1834	11 Q9EO59	Q9e059 rattus norv
20	174.5	6.6	1688	13 Q57483	Q57483 rana catesb
21	172	6.5	2169	11 Q92305	Q92305 cavia porce
22	171	6.5	2288	11 Q9WUB8	Q9wub8 rattus norv
23	171	6.5	2295	11 Q9WUT2	Q9wut2 mus musculu
24	170	6.5	1351	11 Q02789	Q02789 mus musculu
25	170	6.5	2435	5 Q9W433	Q9w433 drosophila
26	169.5	6.4	1536	4 Q9NY44	Q9nyy4 homo sapien
27	169.5	6.4	2373	4 Q96R29	Q96rt9 homo sapien
28	168.5	6.4	2333	11 Q89089	Q89089 rattus norv
29	168	6.4	751	13 Q90Z28	Q90z28 sternopygus
30	167.5	6.4	1791	4 Q9UHB0	Q9uhe0 homo sapien
31	167.5	6.4	1791	4 Q9U133	Q9u133 homo sapien
32	167.5	6.4	1981	4 Q9NZC8	Q9nzc8 homo sapien
33	167	6.3	1715	5 Q18840	Q18840 caenorhabdi
34	167	6.3	1765	11 Q9R053	Q9r053 mus musculu
35	167	6.3	1837	5 Q967R4	Q967r4 caenorhabdi
36	165	6.3	1518	5 Q963J6	Q963j6 schistosoma
37	164.5	6.2	588	11 Q91ZP5	Q91zpz mus musculu
38	164	6.2	2506	4 Q9NS88	Q9ns88 homo sapien
39	163.5	6.2	1740	5 Q17314	Q17314 cyanea capi
40	163.5	6.2	1956	4 Q9Y5Y9	Q9y5y9 homo sapien
41	163	6.2	2365	11 Q9JKB5	Q9jkb5 mus musculu
42	162.5	6.2	2146	13 Q9PUM3	Q9pum3 gallus galli
43	162.5	6.2	2321	13 Q9PUM4	Q9pum4 gallus galli
44	162	6.2	414	4 Q96P54	Q96p54 homo sapien
45	162	6.2	528	4 Q96P56	Q96p56 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9NT82	PRELIMINARY;	PRT;	371 AA.
AC	Q9NT82;			
DT	01-OCT-2000 (TREMBLERel. 15, Created)			
DT	01-OCT-2000 (TREMBLERel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLERel. 19, Last annotation update)			
DE	HYPOTHETICAL 42.5 KDA PROTEIN (FRAGMENT).			
GN	DKF2P434M0223.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RA	Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;			
RL	Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; ALJ37479; CAB70760.1; ..			
DR	InterPro; IPR000636; Cation_chan_non_lig.			
DR	InterPro; IPR002111; Cat_channel_Trip.			
DR	InterPro; IPR001682; Channel_pore_Ca_Na.			
DR	Pfam; PF00520; ion_trans; 1.			
KW	Hypothetical protein.			
FT	NON_TER			
SO	SEQUENCE			
Query Match	371 AA; 42546 MW; F01113FFPD4E35B2 CRC64;			
Best local Similarity	99.6%; Score 1180; DB 4; length 371;			
Matches	222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	263 WRPEWGLSLMDMTRLMLTLVRFRLRIIPSMKPAVAVSVVLGVQMKRAFGGLVVY			322
DB	149 WRPEWGLSLMDMTRLMLTLVRFRLRIIPSMKPAVAVSVVLGVQMKRAFGGLVVY			208
QY	323 YVVFALIGINLFRGYVALPAGNSLAPANGSPCGSEFQLEYWANNFDFPAALVTLWN			382
DB	209 YVVFALIGINLFRGYVALPAGNSLAPANGSPCGSEFQLEYWANNFDFPAALVTLWN			268

QY 363 MYVNMQVFLDARYRSCPSWKIYFVLMVSSVIMVNFLLALLIENFLHKKWDPKSHLP 442
 Db 269 MYVNMQVFLDARYRSCPSWKIYFVLMVSSVIMVNFLLALLIENFLHKKWDPKSHLP 328
 QY 443 LAGTPEATYOMTVELLFRDILEEPDELETERLSOPHMLCR 485
 Db 329 LAGTPEATYOMTVELLFRDILEEPDELETERLSOPHMLCR 371

RESULT 2

O9WTN5 PRELIMINARY: PRT: 819 AA.
 ID O9WTN5
 AC O9WTN5.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE VOLTAGE-GATED CA CHANNEL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=20218667; PubMed=10753632;
 RA Ishibashi K., Suzuki M., Imai M.;
 RT "Molecular cloning of a novel form (two-repeat) protein related to
 RT voltage-gated sodium and calcium channels.";
 RT Biochem. Biophys. Res. Commun. 270:370-376(2000).
 DR EMBL: AB018253; BAA76556.1;
 DR InterPro: IPR000636; Cation_chan_non_1lg.
 DR InterPro: IPR002111; Cat_channel_trpl.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans_2.
 DR PROSITE: PS00307; IECTIN_LEGUME_DFTA; UNKNOWN.1.
 SQ SEQUENCE 819 AA; 94609 MW; A9D3ABAC37BF9E3 CRC64;

Query Match 13.1%; Score 345; DB 11; Length 819;
 Best Local Similarity 25.7%; Pred. No. 4.5e-21;
 Matches 117; Conservative 71; Mismatches 164; Indels 104; Gaps 18;

QY 60 YFQNPESLTLVLTANNPDVMIIPAYSKNRAIAFFIVTVIGSLFLMNLIAIYS 119
 Db 263 YFNTLNSIVNLEVLTTANPEVDMPSISRNPMSCVEFIYSLIELYFIMMLAVVD 322
 QY 120 QFRGIAMSLQSLFRRLGTRAFELVSSWEGEGAF-----POATRGPEST 167
 Db 323 TFNDLEKHKFKSLHKKRTAIOHAYHLVSOQRPAIGISYRQEGIMRFYKPKMSARE--- 379
 QY 168 SLRRCRADSSSSATTTLT-----WGTSSPWQTW---CPFACSWCMQMCC 210
 Db 360 --RFTLFRALNQSNTPPLSLKDFYDIEVAALQWRAKKRQHPDELPTAFILFKG--- 434
 QY 211 LLSVNTSSMGFSASLCTT---CW-----SCCSRSLPACESTCTPATCLT- 255
 Db 435 -INILVNSKAFQYFMYLVAVANGVILVETMLKGNISKHVPWSY-----LVFLTI 486
 QY 256 -----GSSPL-----SCWRP-----EWGLSLMDMTMLNK-----LIVER- 287
 Db 487 YGVELFMVAVAGIPVEYLSGGMNLFDFSLTAFAFGLIAL-----TIMNEPFFYIVLRP 541
 QY 288 --FLRIITSMKPMVAVSTVLGLVONMRAFGIILVYVYVAIIGINLFRGVI---VALP 342
 Db 542 LQLLTLFLKRYRNVLDLTMELLPRMASLGLTLTFYSAIVGMEFFSGRLSPNCSTP 601
 QY 343 GNSSLAPANGS-APCGSEPOL-----EYMANNDDEFAALVLTMLNMYNNQVFLDARR 397
 Db 602 ARWGILTPIDSSITRLGNKTKGRKGYLYLNNDNLINSFVTLFELTVANNMIIIMEGVS 661
 QY 398 YSGPWSKIYFVLMVSSVIMVNFLLALLIENFLH 433
 Db 662 QTSKHSRLYFMETFYIVTMV--MTIIVAFILAEFVR 696

RESULT 3

O92T83 PRELIMINARY: PRT: 724 AA.
 ID O92T83
 AC O92T83.
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE CALCIUM CHANNEL.
 GN F9H3.19 OR T5L23.5 OR A74G03560.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Huang E.N., Parnell L.D., de la Bastide M., Schutz K., Habermann K.,
 RA Dedhia N.N., McComble W.R.;
 RT "Genomic sequence of Arabidopsis Thaliana BAC F9H3, chromosome IV,
 RT 18.8 cm.";
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
 RT "BAC F5L23 from chromosome IV, position 19 cm.";
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
 RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
 RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 DR EMBL: A071527; AAD15312.1;
 DR EMBL: A071527; AAD15312.1;
 DR EMBL: AL161497; CAB77841.1;
 DR InterPro: IPR000636; Cation_chan_non_1lg.
 DR InterPro: IPR002111; Cat_channel_trpl.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR003015; HLH_Myc.
 DR InterPro: IPR001696; Na_channel.
 DR Pfam: PF00036; ehand; 2.
 DR Pfam: PF00520; Ion_trans; 2.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SMO0054; EFh; 2.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN.1.
 KW Calcium-binding.
 SQ SEQUENCE 724 AA; 83856 MW; EBA3A27EB15BEF32 CRC64;

Query Match 13.0%; Score 342; DB 10; Length 724;
 Best Local Similarity 24.1%; Pred. No. 7e-21;
 Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;

QY 55 RERLTYFQNPESLTLVLTANNPDVMIIPAYSKNRAIAFFIVTVIGSLFLMNLIT 114
 Db 233 QOGLTVFTSYGATLYQMFILFTTSNNPDVMIIPAYKSSRWSSVFVLYVLIGVYFTNITL 292
 QY 115 AIYSGFQGLYLMKSLQ-LSLFRRLGTR-----AFEVLS----- 149

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Db 293 AAYYDSKEQOLAKOVSGMDQMRRLKARGLIDSDKNGEIDKNGQIKLFEQLINRYTLR 352
OY 150 --MWGEGA-----PQATRGPST 167
Db 353 KISKEEGLFDELDTRDKINKDEFADLCQALALRFOKEVPSLFHEHPQIYHSALSQ 412
OY 168 SLR-FCRAPSSSA-----TTTLTWGTS--PMQTMCPACSMCM-MQMC 209
Db 413 QLRFAVSPNFGYALISFLINFIYAVVETLIDIESSAKPMQV-AEFGWYIVLEMA 471
OY 210 CLLSVMT-----SSW--GFSTASSLCTTCWSCSRLPACGEGTPTPATCLTGSSPLSCW 263
Db 472 --LKITYGFEENYWRGANGREFLVY-----WVI--VIGETATFT----- 508
OY 264 RPEWGLSLMDTQMLNMLIVFRFLRIPSMKPMNAVASTVLGYNOMKAFGLIYVY 323
Db 509 -PDENFFSGEWIRYLLARMLRLILMNVOYRAFIYFTLPLSLMPYLGTFICVL 567
OY 324 YVFAIIGINLFRGVIALPGNSSLAPANGSAPGSGFE---OLEYMANPFDFPAALVTL 379
Db 568 CICYSIGVOYFGGLVNA--GNKKL-----FETELADEDYLLFNNDYVNGMYTL 614
OY 380 WNLVAVNNVOYFLDARYRSGPMSKI-YVILMVLSSVIYVWNLFLALILENLEHKWD 435
Db 615 FNLLVGNMVOYMWESYKDLGTWMSITYEVSFYVITILLNLNVAVLEAFTEELD 671

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RESULT 4
O94K18 PRELIMINARY: PRT; 733 AA.
AC O94K18:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE PUTATIVE CALCIUM CHANNEL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Fischer M., Knight H., Amtmann A., Sanders D.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF360372; AAK39534.1;
SQ SEQUENCE 733 AA; 84873 MW; 1CA978DB68BFF445 CRC64;

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Query Match 13.0%; Score 342; DB 10; Length 733;
Best Local Similarity 24.1%; Pred. No. 7.1e-21;
Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;
OY 55 RERLTFPQNLPELSLTLVLTANNPDVMIIPAYSKNRAVAFFIYFVIGSLFNLTLT 114
Db 242 QOGLTFVTSYGATLQOMFLFTSNPDVMIIPAYSKSRMSVFFVLYVILGYFVNLTL 301
OY 115 AIYISQFGLYLMKSLQ-TSLFRRLGTRA-----AFEVLS----- 149
Db 302 AAVYSFEKEQLAKQVSGMDQMRRLKARGLIDSDKNGEIDKNGQIKLFEQLINRYTLR 361
OY 150 --MWGEGA-----FPQATRGPST 167
Db 362 KISKEEGLFDELDTRDKINKDEFADLCQALALRFOKEVPSLFHEHPQIYHSALSQ 421
OY 168 SLR-FCRAPSSSA-----TTTLTWGTS--PMQTMCPACSMCM-MQMC 209
Db 422 QLRFAVSPNFGYALISFLINFIYAVVETLIDIESSAKPMQV-AEFGWYIVLEMA 480
OY 210 CLLSVMT-----SSW--GFSTASSLCTTCWSCSRLPACGEGTPTPATCLTGSSPLSCW 263
Db 481 --LKITYGFEENYWRGANGREFLVY-----WVI--VIGETATFT----- 517
OY 264 RPEWGLSLMDTQMLNMLIVFRFLRIPSMKPMNAVASTVLGYNOMKAFGLIYVY 323

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Db 518 -PDENFFSGEWIRYLLARMLRLILMNVOYRAFIYFTLPLSLMPYLGTFICVL 576
OY 324 YVFAIIGINLFRGVIALPGNSSLAPANGSAPGSGFE---OLEYMANPFDFPAALVTL 379
Db 577 CICYSIGVOYFGGLVNA--GNKKL-----FETELADEDYLLFNNDYVNGMYTL 623
OY 380 WNLVAVNNVOYFLDARYRSGPMSKI-YVILMVLSSVIYVWNLFLALILENLEHKWD 435
Db 624 FNLLVGNMVOYMWESYKDLGTWMSITYEVSFYVITILLNLNVAVLEAFTEELD 680

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RESULT 5
O94UQ1 PRELIMINARY: PRT; 775 AA.
AC O94UQ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE KIAA1169 PROTEIN (FRAGMENT).
GN KIAA1169.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RL from size-fractionated cDNA libraries from human brain.";
DR EMBL, AB032955; BAA86483.1;
DR InterPro: IPR000636; Cation_chan_non_119.
DR InterPro: IPR002111; Cat_channel_TrypL.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001220; Lectin_legB.
DR InterPro: IPR001696; Na_channel.
DR Pfam: PF00520; ion_trans_2.
DR PRINTS: PRO0170; NACHANNEL.
DR PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
FT NON-TER
SQ SEQUENCE 775 AA; 90039 MW; 7084CC9A7F62E85 CRC64;

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Query Match 13.0%; Score 342; DB 4; Length 775;
Best Local Similarity 25.4%; Pred. No. 7.6e-21;
Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;
OY 60 YFQNLPELSLTLVLTANNPDVMIIPAYSKNRAVAFFIYFVIGSLFNLTLT 119
Db 221 YSTLENSIVSLFVLTANNPDVMIIPAYSKSRMSVFFVLYVILGYFVNLTL 280
OY 120 QRGYLMKSLQSLFRRLGTRAFAEVLSMNGEGGAFPOATRRGPSTLRCRAPSSSS 179
Db 281 TFNDIEKRKFSLLMKRTAIOHAYRLISORRPAQ---ISYRQEGMLRFEYK-PRMSA 335
OY 180 ATTTLT-----TWGSSPMQTMCPACSMCMQKCLL- 212
Db 336 RERLTFPQNLPELSLTLVLTANNPDVMIIPAYSKNRAVAFFIYFVIGSLFNLTLT 389
OY 213 --SVMTSSWGFSTASSLCTT--CW-----SCGSRLPACGEGTPTPATCL 254
Db 390 FGINIIVSKAFQYFMYLVAVNGVILVETFMKLGNGFSGHVPWS-----LVFL 442
OY 255 T-----GSSRL-----SCMRP-----EAVGLSLMDTQMLNML- 286
Db 443 TIYGVLELKAVALGQVYELSSGMNLFDSVTFVAFGLIAL-----ALNMPFFYIVVL 497
OY 287 R---FLRIPSMKPMNAVASTVLGYNOMKAFGLIYVYVFAIIGINLFRGVIALPG 343
Db 498 RPIQGLRFLFKLKERIRYVLDITFELLPRAASIGLITLLITYYSFAIYVNGEFGIYVPMCC 557

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OY 344 NSSLAP-----ANGSAPCGSFQOLEYANNFDDFAALVTLMLNMLVNNMNOVED 393
DB 558 NSTSVADAYRMRNHYGNRTV-----VEEGYILNFDNLINSFVTLFELTYVNNMYIME 613
OY 394 AYRRYSGPWSKIYFVLMVLVSVYVWNLFLALILENLELHK 433
DB 614 GVTSTQSHMSRLYEMTFEYITVMV-MTIIIVAFLEAFVR 652

RESULT 6
O9EQJ0 PRELIMINARY: PRT: 817 AA.
ID O9EQJ0:
AC O9EQJ0:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCIUM CHANNEL.
GN CALCIUM CHANNEL.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HE;
RA "Perlygin A.A., Brinton M.A.;
RL "Positional cloning of the Flv gene."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217002; AAC44100.1;
DR InterPro: IPR000636; Catlon_chan_non_119.
DR InterPro: IPR002111; Cat_channel_TPL.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001220; Lectin_legb.
DR Pfam: PF00520; Ion_trans_2.
DR PROSITE: PS00307; LECTIN_LEGOME_BETA; UNKNOWN_1.
DR PROSITE: PS00307; LECTIN_LEGOME_BETA; UNKNOWN_1.
SQ SEQUENCE 817 AA; 94496 MW; 269930EID1136E10 CRC64;

Query Match 13.0%; Score 342; DB 11; Length 817;
Best Local Similarity 25.3%; Pred. No. 8e-21;
Matches 117; Conservative 70; Mismatches 156; Indels 120; Gaps 18;

OY 60 YFQNLPSLSLVLTLTANNPDVMPAYSKNRAIYFVYVIGSLFLMLNLTAIYS 119
DB 263 YFSLNLSIVLFLVLTANPDVMPSPVSNPMSVCEFFVYLSIELYFIMNLILAVFD 322
OY 120 QERGLKSLQTSFRRRLGTRAFVYSSWVGEGAF-----POATRRGPT 167
DB 323 TFNDLEKHKFKSLHLKRTAIGHAYGILASORRAGISYFQESLMRFYPRMSAR 379
OY 168 SLRRCRAFSSTSTTTLT-----WGTSPPQWT---CPFACSMCMQMC 210
DB 380 --RELTFKALNQSWTPLSLKDFYDIYVALQWAKARNRQHWDELPRFAFLFKG 434
OY 211 LLSVWTSWGFSSTSLCTT---CW-----SCGSSLPWACBGCPPTATCLT 255
DB 435 -INILVNSKAFQYEMYLVAANGVWILVEFPMKLGKNTSKHYWST-----LVFLTI 486
OY 256 -----GSSPL-----SCMRP-----EMVGLSLMDMTMLNM-----LIVER 287
DB 487 YGVELFMVAGLGPVEYISGWNLEFDSVTAFELGLLAL-----TLNMEFYIVLRP 541
OY 288 --FLRIIPSMKPMVAVASTVLGLVONNRAGGILLVVIYFAIIGLINFRAVIALGNS 345
DB 542 LQTLRLFKLKKRYRNVLDITMELLPRMASLGLTLTFEYSPFAIVGMEFF-----NG 592
OY 346 SLAP--ANGSAPCGSF-----BOLEYANNFDDFAALVTLMLNMLVNNMNOV 390
DB 593 RLTPPCCTSTVADAYRMRNHYGNRTV-----VEEGYILNFDNLINSFVTLFELTYVNNMYI 652
OY 391 FLDAAYRRYSGPWSKIYFVLMVLVSVYVWNLFLALILENLELHK 433
DB 653 IMEGVTSQTSQSHMSRLYEMTFEYITVMV-MTIIIVAFLEAFVR 694

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RESULT 7
O948T1 PRELIMINARY: PRT: 733 AA.
ID O948T1:
AC O948T1:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TWO-PORE CALCIUM CHANNEL.
GN ATPPC1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RC MEDLINE=21461266; PubMed=11577183;
RX Furlichi T., Cunningham K.W., Muto S.;
RA "A putative two pore channel ATPPC1 mediates Ca2+ flux in Arabidopsis
RT leaf cells."
RL Plant Cell Physiol. 42:900-905(2001).
DR EMBL; AB053952; BAB55460.1;
SQ SEQUENCE 733 AA; 84872 MW; 490937356172E80C CRC64;

Query Match 12.8%; Score 336; DB 10; Length 733;
Best Local Similarity 23.9%; Pred. No. 2.3e-20;
Matches 114; Conservative 84; Mismatches 145; Indels 134; Gaps 19;

OY 55 RRLRYFQNLPSLSLVLTLTANNPDVMPAYSKNRAIYFVYVIGSLFLMLNLTAIYS 114
DB 242 OQGLTVFTSYGATLFOMLTFTSNPDVMPAYSKNRSWSSFFVLYLVIGYVYTNLIL 301
OY 115 AIIYSGFGLYKSLQ--TSLFRRRLGTRAF-----AFEVLS----- 149
DB 302 AYVYDSFKQGLAKQYSGMDQMKRRMLEKAFGLIDSKNGEIDKQCKLFLQLTNYRLP 361
OY 150 --WVGEGA-----PQATRRGPT 167
DB 362 KISKKEFGILFDELDTDRFKINKDFADLCQALRQKEVPSLFEPQIYHSLSQ 421
OY 168 SLR-FCRAPSSSA-----TTTLTWTGSS--PMQWCPFACSMCW-MQMC 209
DB 422 QLRAPFSNPGYALISFILLTFIYAVVETITDIESSAQKRWQ-AEFVGMIVLEMA 480
OY 210 CLLSVWT---SSW--GFSTASSLCTTCWSCCSRLPWAACETCTPATCLTGSSPLSCW 263
DB 481 --LKIYTGFEVNWREGANRFDELVT-----WVI--VIGETATFTT----- 517
OY 264 RPEWGLSLMDMTMLNLILYFRRLIIPSKPMVAVASTVLGLVONNRAGGILVYV 323
DB 518 -PDENTFFSNGEWIRTLRLARMLRLTLMANQRRARAFATITTLIPSLMPLGLITPCVL 576
OY 324 YVFAIGILNFRGVIALPGNSLAPANGSAPCGSFE-----OLEYANNFDDFAALVTL 379
DB 577 CIYCSIGQYFGGLVNA--GNKKL-----FETELADVDYLLFFNDYPRGNVTL 623
OY 380 WNLVNNMNOVELDAYRYSRSGPWSKI-YFVLMVLVSVYVWNLFLALILENLELHKWD 435
DB 624 FNLLVGNQNMWMEYSKDLGTWMSITVFSEYVITILLNLVVAFLVLEAFTELD 680

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RESULT 8
O91WX9 PRELIMINARY: PRT: 1643 AA.
ID O91WX9:
AC O91WX9:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VOLTAGE-GATED CALCIUM CHANNEL PORE FORMING SUBUNIT CANV1.3ALPHA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
 RX MEDLINE=21380268; PubMed=11487617;
 RA Xu W., Lipscombe D.;
 RT "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively
 RT hyperpolarized membrane potentials and are incompletely inhibited by
 RT dihydropyridines";
 RL J. Neurosci. 21:5944-5951(2001).
 DR EMBL: AF370009; AAK72959.1;
 SQ SEQUENCE 1643 AA; 186828 MW; 97AAA34B073EA520 CRC64;

Query Match 7.6%; Score 201; DB 11; Length 1643;
 Best Local Similarity 18.2%; Pred. No. 2, 1e-08;
 Matches 93; Conservative 82; Mismatches 174; Indels 162; Gaps 17;

OY 12 CRGGGMVPTGWVRLGELSLMGDDPYVPMSCRFCSQDDGQDRERLTYPQNLPESLTSL 71
 Db 324 CR--SGVVGPNGGI-----TTFDNPFAMLTV 348
 OY 72 LVLTITANNPVMIPAYSKNRAYA-----IFETIVYIGSLFNLNLTAIYSQFRTLM 126
 Db 349 FQGITMGMTDVL--YVWDALGEMPMWYEVYSLITLGSFVNLVLGLSGF----- 400
 OY 127 KSIQTSIFRRRLGTAAFEVLS-----MVGEGAFPOATRGRPSTSLRFC 172
 Db 401 -----SKERKAKARGFQKIREKQOLEEDLKGYLDWITQAEIDIDPENEGGEGKRN 455
 OY 173 RAPSSSATTTLTWGTSSPMQWCPACMCWMOCCILSVMTSS--WGFSTASSLCT 229
 Db 456 SMTSE--TTSVNTENVSGGEGTGGCCGLMCWMMKRRGAATGPGRCRWGAISKSL 513
 OY 230 TCWSSCSRLPMACEGTCTPA-----TCLTSSP----- 259
 Db 514 RRRRRNRNRRRRRAAVKSVTFYWLIVLVLNLTLSSEHNQDPWLQIODIANKYL 573
 OY 260 LSCMRP-----VGLLSIMD-----TRMLNMLTV-----FR 287
 Db 574 LALFTCEMLVKMTSLQIAVFSLFNRFDFVVCGGITETILVELLSPLGVSFRCVR 633
 OY 288 FLRIIPSMKPMAYASTVLGIYONMRAFGIIVVY--VFALIGNLFRGYVALPGN 344
 Db 634 LRIFFVTRHMTSLSLNVLVSLNMSKSLSLILFLFTITSLTGMOQFGK----- 687
 OY 345 SSILAPNGSAPCGSEFOLEYMANNFDAALVTLMNVNMO--VELDAYRRYSGPMS 403
 Db 688 -----NFEDETQTKRSTFENFPQALLTFQILGEDMNVAMVDGIMAYGSPS 734
 OY 404 K-----YFVLMWLVSVIWNLFALILEN 429
 Db 735 SGMIVCIYIIFIGCNITLLNVLAIADVN 765

RESULT 9

O923K6 PRELIMINARY; PRT; 2295 AA.
 ID O923K6
 AC O923K6
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CALCIUM CHANNEL ISOFORM ALPHA1.7.
 GN CAV2.3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Mitchell J.W., Larsen J.K., Best P.M.;
 RT "Identification of the Calcium Channel alpha1e (Ca2.3) Isoform

RT Expressed in Atrial Myocytes";
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY029412; AAK33009.1;
 SQ SEQUENCE 2295 AA; 259227 MW; 7AE2D2DEC30E64F CRC64;

Query Match 7.3%; Score 191.5; DB 11; Length 2295;
 Best Local Similarity 22.2%; Pred. No. 2e-07;
 Matches 105; Conservative 79; Mismatches 187; Indels 103; Gaps 20;

OY 32 LMGGPVVPMSCRFCSQDDGQD-----RERLTPQNLPESLTSLVLTANNPVMIPA 87
 Db 259 LEGPDPHPPCVQCGPAPAECKDWIGPDGTFQDFNLPAVLTVFQGITMGMTVL--- 315
 OY 88 YSKNRAYA-----IFETIVYIGSLFNLNLTAIYSQF-----RGYMKSLQTS 132
 Db 316 YNTNDALGATWNLVFIPLIITLISFVNLVLGLSGFAERERENRRAPFKLRQO 375
 OY 133 LERRRLGTAA-----AFEVL--SMVGEAGAFPOATRGRPSTSLR--FCRAPSSSATTTL 184
 Db 376 IERELNGTRAWIDKAEVYMLAEKNKSGTSALEVLRRATIRKSRTEAMTRDSDHECVDI 435
 OY 185 TTWGT---SSPMQWCPACMCWMOCCILSV--MTSS--WGFSTASSLCTTQMSC 234
 Db 436 SSVGTPLARASIKSTKVDGASYFRHKERLRLSIRHWKSGVFYIYLVVALNTACVAT 495
 OY 235 CSRSLP-WACE-----GTCPPTATCLGSSPLSCWR--PENYGL 270
 Db 496 VHNQPPQWHLHLYAEFLGLFLMLSKMYGMGR---LYHSSFNCFDEGVTVGS 551
 OY 271 L--SLAMQTRM-----LNLIVFRRLIIPSMKPMAYASTVLGIYONMRAFGIIVVY 323
 Db 552 IFEVYMAIFPRGTGFGSLVLRALRLRIKTKYMASIRNLVYLSMSKSLITLFLFL 611
 OY 324 ---YFAIIGNLFRGYVALPGNSILAPNGSAPCGSEFOLEYMANNFDAALVTLM 380
 Db 612 LFTVFFALDMQLEFGRFNFDGTPSA-----NDFEPAAIMTF 651
 OY 381 NIMVNVNM--QVFLDAYRRY---SGPMKTYFVLMWLVSVIWNLFALILEN 429
 Db 652 QILGEDMNEVLNGLIRSGGSSGMSAIFYVLTLLNGYTLNVLAIADVN 705

RESULT 10

O91W25 PRELIMINARY; PRT; 1602 AA.
 ID O91W25
 AC O91W25
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA1 SUBUNIT.
 GN CAV1.3 (ALPHA1D).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 RN NCBI_TaxID=10036;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HIT CELL;
 RX MEDLINE=21329586; PubMed=11435619;
 RA Schnolze A., Plant T.D., Dolphin A.C., Nuerberg B.;
 RT "Functional expression and characterization of a voltage-gated Cav1.3
 RT (alpha1d) calcium channel subunit from an insulin-secreting cell
 RT line";
 RL Mol. Endocrinol. 15:1211-1221(2001).
 DR EMBL: AJ311617; CAC48390.1;
 SQ SEQUENCE 1602 AA; 181297 MW; 4207378974DE2456 CRC64;

Query Match 7.2%; Score 190; DB 11; Length 1602;
 Best Local Similarity 17.9%; Pred. No. 1.8e-07;
 Matches 91; Conservative 87; Mismatches 173; Indels 158; Gaps 18;
 OY 6 WEATGR-CRLGG-----GMVPTGWVRLGELSLMGDDPYVPMSCRFCSQDDGQDRERLT 59

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Db      310 FSGNRQCAVNGTECRSGWGPNGI-----T 336
QY      60 YQONLPESITSLVLTANNPDVMI PAYSKNRAYA-----IFVFTVIGSLFLMLNLT 114
Db      337 NFDNRAFAMLVFQCITHEGWDVL---YMNDAAGFELPMVYFVSLVIFSGFVLNVL 393
QY      115 AIYISOFRGLYMKSLQTSLFRRLCTRAAEVLSMVG-----EGAFPOA 160
Db      394 GVLSGEFSKERERAKARGFOKLRKQOLEEDLKGYLDMITQOEDIDENEEGEGEGR 453
QY      161 TRRGSTSLRRCARAPSSSATTLTWTG-----SSPMQWCF-----A 200
Db      454 NTSMPSTSESYNTENVSCEGFCGSCSLCAISKSLSRKRNKRNRRRCNAAVKS 513
QY      201 GSCWMMQCL-LSVMTSS-----WGF-----STASSICTTQWSC-----CSRSLP-- 240
Db      514 VFFYWLVIYLVLFNTLTISEHYNOPDMLTQIODIANKVLALFTCEMLVKMYSGLQAY 573
QY      241 -----WAGETCTPATCLTGSPLSCWPREMVGSLTMDMTMLMLIVFRPL 289
Db      574 FVSLFRNRCDFVCGGITFILLVLELMSPLG-----VSFRCVRL 615
QY      290 RIIPSKPAAVAVSYVLGVONMRAFGILVYV---YVFAIIGINLFRGIVALPGNSS 346
Db      616 RIFKVRHMTSLNVLASILNKSJASLILLLFLLIFSLIGMQLFGGRF----- 667
QY      347 LAPANGSAPCGSEOLEYANNEDFAALVTLMLMAYVNNQ-VFLDAYRYSQPMK- 404
Db      668 -----NDEFTQTRSTDFNPQALTVFOILTGEDMNAVYDGMAYGGSSSG 716
QY      405 -----YFVLMWLVSSVYVWLFLALLEN 429
Db      717 MIVCITFILLICGNITLLNVLAIADN 745

RESULT 11
ID 096057 PRELIMINARY; PRT: 2125 AA.
AC 096057;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ASCIDIAN CALCIUM CHANNEL ALPHA-SUBUNIT.
GN TUCAL.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamura Y., Okagaki R.;
RT "Tucal, ascidian calcium channel alpha-subunit.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB013604; BA34527.2; -.
DR InterPro: IPR000636; Cation_chan_non_1ig.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR002077; Ca_channel.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001696; Na_channel.
DR Pfam; PF00520; ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR00170; NACHANNEL.
SQ SEQUENCE 2125 AA; 242981 MW; 7C8B25B37A10FC0 CRC64;

Query Match 7.2%; Score 189.5; DB 5; Length 2125;
Best Local Similarity 20.2%; Pred. No. 2,7e-07;
Matches 99; Conservative 76; Mismatches 159; Indels 157; Gaps 20;

QY 33 WGGDVVWSCRFCG-----QDDGQDERLTYFQNLPESTLSLVLTANNPDVMI 87
Db 234 WC-----RHGSGGICESDMAGPSKGIINFTGYFAVITVFOCITMGWDVL--- 281

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QY      88 YSKNRAYA-----IFVFTVIGSLFLMLNLTAAIYSOFRGLYMKSLQTSLFRRLCTRA 142
Db      282 YVANDAVGNLMPWITVYFSLIISFFVMNLLGLGEE-----SKEREKMANAG 331
QY      143 AFEVL-----SSWGECAFPQATRGP-----STSLRRCAPSSSATTL 184
Db      332 EFOKLRKQOTDEDMKGYMDWITQADLDPMNDEDEDRRSASNEOLNDSFVSLQID 391
QY      185 TWTWT-----SSPMQW-----CPE-----ACSCWMMQ-----CCLSVMTSSM 219
Db      392 EYMWQORRALFKVCYRRRRNRKRRCRRMVKVSKSYWLVYLVFCNTSLATEHY 451
QY      220 GFSTASSICTTQWSCSRSLPWACEGTCPPATCLTGSPLSCWRDE----- 267
Db      452 -----RPPWL-----TIAODLANKILLFTTEMLVKMYSIGMOQY 488
QY      268 -VGLSLMD-----MPEM-----LNMLIVFRFLRISMKPAAVAVSYVLG 307
Db      489 FVSLFRNRCDFVCGGIVELVLTSSKIMEPLGISVLRGVALLIFKMTSSMNSLNLVAS 548
QY      308 LVQNMRAFGILVYV---YVFAIIGINLFRGIVALPGNSSLAPANGSAPCGSEQLEY 364
Db      549 LNSIRSIASLVLLFLLIFLALGMQMGGRF-----SEIRQEDK 590
QY      365 WANNEDFAALVTLMLMAYVNNQV-----LDAYRYS--GPMKIFYVLMWLVSSVW 418
Db      591 IRSNEDFLQALTVFOILTGEDMNAVYNGIEYVGAISTIGLITVYFVLPFGNVL 650
QY      419 VNLFLALLEN 429
Db      651 LNVFLAIADN 661

RESULT 12
ID 095226 PRELIMINARY; PRT: 1912 AA.
AC 095226;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.
GN CACNA1F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bech-Hansen N.T., Naylor M.J., Maybaum T.A., Pearce W.G., Koop B.,
RA Fishman G.A., Mets M., Musarella M.A., Boycott K.M.;
RT "Loss-of-function mutations in a novel retinal gene in xpl1.23 cause
RT incomplete CSNB.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067227; AAD03587.1; -.
DR InterPro: IPR000636; Cation_chan_non_1ig.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR002077; Ca_channel.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR Pfam; PF00520; ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR00167; CACHANNEL.
SQ SEQUENCE 1912 AA; 214031 MW; 0E2C45C8B4156E0D CRC64;

Query Match 7.2%; Score 189; DB 4; Length 1912;
Best Local Similarity 18.3%; Pred. No. 2,7e-07;
Matches 102; Conservative 79; Mismatches 157; Indels 220; Gaps 22;

QY 4 ACWEATGRCRLGGGNNVPTGWRGLSLMGDPVYVWSCRCSQDDQDQDERLTYCN 63
Db 226 ACTLNGTECR--GRWGPNGI-----TNDN 250
QY 64 LPSLISLVLTANNPDVMI PAYSKNRAYA-----IFVFTVIGSLFLMLNLTAL 118
Db 251 FFFAMLVFQCITHEGWDVL---YMNDAAGFELPMVYFVSLVIFSGFVLNVLGVL 307

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QY 119 SOF-----RGYLMKSLQTSFERRRLGTRAEVLSMWG 152
 Db 308 GEFSEKEREKAKRGDFOKOREQOEEDLRYL--DWITQAEELMEDPESADNDGSMAE 365
 QY 153 EG--GAPFOAT-----RGPSTSLRF-----CRAPSSSATTTLTWTGSSPWQW----- 196
 Db 366 EGRAGHRPOLAEELTNRRG--RLKWFHSHSTRSHSTSHSLPASPDTGSMETGDEDE 422
 QY 197 -----C-----PFACSMC----- 204
 Db 423 EGALASCTRCINKIMKTRVGRRLRANRVLARCRRAVKSACWAVALLVFLNTLTIA 482
 QY 205 -----WMO-----MCCLISV--MTSSWGFSTASSICT-----TCMSCCSRSLP 240
 Db 483 SEHGQPVWLQIOEYANKVLLCFTVEMLTKLYGLGPSAYVSPFNREDFVCG----- 538
 QY 241 WACBGTCTPATCLTGSSPLSCWREPMYGLSLMDMTMLNMLYERFLRIIPSKPMAY 300
 Db 539 -----GILETTIVEGAMQPLG-----ISVLRVRLIRIKYTRHMAS 576
 QY 301 VASTVLGLVQNMRAFGLVYVY---YFAIIGINLFRGVIALPONGSLAPANGSAPCG 357
 Db 577 LSNLVASILNSMKSIASILLFLFIIFSLGMLFGGKF----- 617
 QY 358 SFEOLEYANNFDDPAALVTLMLNMYVNNQVFL--DAYRRYSGWSK-----IYFVLMW 411
 Db 618 NFDQTHRKRSFTDFPQALLTVFOILTGEDMNVVYDGMAYGPFPGMLVCIFYILLF 677
 QY 412 LVSSVIWVNLFLALLEN 429
 Db 678 ICGNTILLNVLALAVDN 695

RESULT 13

09UHB1

ID 09UHB1 PRELIMINARY: PRT: 1977 AA.

AC 09UHB1
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20334628; PubMed=10873387;
 RA Naylor M.J., Rancourt D.E., Bech-Hansen N.T.,
 RT "Isolation and Characterization of a Calcium Channel Gene, Cacna1f,
 RT the Murine Orthologue of the Gene for Incomplete X-Linked Congenital
 RT Stationary Night Blindness."
 RL Genomics 66:324-327(2000)
 DR EMBL: AF201304; AAF15290.1;
 DR InterPro: IPR000636; Cation_chan_non_11g.
 DR InterPro: IPR002111; Cat_channel_trpL.
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR InterPro: IPR001696; Na_channel.
 DR Pfam: PF00520; Ion_trans_4.
 DR PRINTS: PR00167; CACHANNEL.
 DR PRINTS: PR00170; NACHANNEL.
 SQ SEQUENCE 1977 AA; 220676 MW; 35433650C6D8E73 CRC64;

Query Match

Best local similarity 18.3%; Score 189; DB 4; Length 1977;

Matches 102; Conservative 79; Mismatches 157; Indels 220; Gaps 22;

QY 4 ACWEATRCRLGGGMVPTGVNRGLSLWGGDPVPMWSCRFCQQODGDQDERLTYFON 63
 Db 291 ACTLNGTECR--GRWPGPNNGI-----TNDN 315

QY 64 LPESLTSLLVLTITANNPDVMIIPAYSKNRAYA-----IFFVEFYIGSLFLNLTITALLY 118
 Db 316 FFAMALTYFOCTMGTMDVLT---YMODAMGYELPWPYFVSLYFGSFLVNLVIGVLS 372
 QY 119 SOF-----RGYLMKSLQTSFERRRLGTRAEVLSMWG 152
 Db 373 GEFSEKEREKAKRGDFOKOREQOEEDLRYL--DWITQAEELMEDPESADNDGSMAE 430
 QY 153 EG--GAPFOAT-----RGPSTSLRF-----CRAPSSSATTTLTWTGSSPWQW----- 196
 Db 431 EGRAGHRPOLAEELTNRRG--RLKWFHSHSTRSHSTSHSLPASPDTGSMETGDEDE 487
 QY 197 -----C-----PFACSMC----- 204
 Db 488 EGALASCTRCINKIMKTRVGRRLRANRVLARCRRAVKSACWAVALLVFLNTLTIA 547
 QY 205 -----WMO-----MCCLISV--MTSSWGFSTASSICT-----TCMSCCSRSLP 240
 Db 548 SEHGQPVWLQIOEYANKVLLCFTVEMLTKLYGLGPSAYVSPFNREDFVCG----- 603
 QY 241 WACBGTCTPATCLTGSSPLSCWREPMYGLSLMDMTMLNMLYERFLRIIPSKPMAY 300
 Db 604 -----GILETTIVEGAMQPLG-----ISVLRVRLIRIKYTRHMAS 641
 QY 301 VASTVLGLVQNMRAFGLVYVY---YFAIIGINLFRGVIALPONGSLAPANGSAPCG 357
 Db 642 LSNLVASILNSMKSIASILLFLFIIFSLGMLFGGKF----- 682
 QY 358 SFEOLEYANNFDDPAALVTLMLNMYVNNQVFL--DAYRRYSGWSK-----IYFVLMW 411
 Db 683 NFDQTHRKRSFTDFPQALLTVFOILTGEDMNVVYDGMAYGPFPGMLVCIFYILLF 742
 QY 412 LVSSVIWVNLFLALLEN 429
 Db 743 ICGNTILLNVLALAVDN 760

RESULT 14

09NYZ6

ID 09NYZ6 PRELIMINARY: PRT: 2224 AA.

AC 09NYZ6
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CALCIUM CHANNEL ALPHA1E SUBUNIT, DELTA39 SPLICED VARIANT
 DE (FRAGMENT).
 GN CACNA1E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miltman S., Agnew W.S., Malek J.A.,
 RT "Exon Organization and Alternative Splicing of CACNA1E."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF233391; AAF37687.1;
 DR EMBL: AF239258; AAF37687.1; JOINED.
 DR EMBL: AF239259; AAF37687.1; JOINED.
 DR InterPro: IPR000636; Cation_chan_non_11g.
 DR InterPro: IPR002111; Cat_channel_trpL.
 DR InterPro: IPR002077; Ca_channel.
 DR InterPro: IPR001682; Channel_pore_Ca_Na.
 DR Pfam: PF00520; Ion_trans_4.
 DR PRINTS: PR00167; CACHANNEL.
 FT NON_TER
 SQ SEQUENCE 2224 AA; 251889 MW; 67D34234924F6690 CRC64;

Query Match

Best local similarity 19.4%; Score 189; DB 4; Length 2224;

Matches 106; Conservative 91; Mismatches 218; Indels 132; Gaps 20;

QY 32 LMGGDPVPMWSCRFCQQODGDQD-----RELTYFONLPESLTSLLVLTITANNPDVMIIP 87

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Db 170 LGGFDPHPCGVGCGPAGYECKDWIGPNDGITQFNDNLFAVLTVFQCITMEGWTVL--- 226
QY 88 YSKNRAYA-----IFFIVTVIGSLFLMNLTAIYSQF-----RGYLMKSQTS 132
Db 227 YNTNDALGATWMLLYFPLIIIGSFVNLVLGVLGSEFAKEREVENRRAFMKLRQOO 286
QY 133 LFRRLGTRAAFEVLSMWEGGAFPOATRPGPSTSLRCPARSSSSATTTTLTWTGSSP 192
Db 287 IERELNGYRAMIDKAEVW-----LAENKNAGTSALEVLRATIKRSTTEMTDSSDE 341
QY 193 W-----QWCPFACS-----WCWMQMCCLSY--MTSS---WGFSTASLCT 229
Db 342 HCVDISSVGTPLARASIKSAKVDGVSFRRKRELRLISIRHMVKSQVFWYIVLSVALNT 401
QY 230 TCWSCCSRSLP-WACE-----GTCPTPATCLTGSSPLSCMR-P 265
Db 402 ACVAIVHNNQPOWLTHLLYYAEFLGLFLLEMSLKNYGMGPR---LYFHSSEFCDFG 457
QY 266 EMVGLL--SLMDMTRM-----LNLIVFRRLIIPSMKPMAYVASTVLGVOMRAFGGI 318
Db 458 VIVGSIIEVVAIFRPGTSEGISVLRALRLRIFKITKWAISLRNLVYSLSMSKSIISL 517
QY 319 LVVVY---YVFAIGINLFRGVIVALPGNSSLAPANGSAPCGSPOLEYMANNEDFPAA 375
Db 518 LFLFLFIVFVALLGMQLFGGRFNFNDGTPSA-----NFDTPPAA 557
QY 376 LVTLMLNVVNNM-OVFLDAYRRY---SGPWSKIYFVLMVLYSSVIVWNLFLALILENF 430
Db 558 IMTFVQILTGEDMNEVMYNGIRSGGVSGMWSAIFYIVLILFGNTTLNVFLAIAVDN 617
QY 431 L-----HKWDPRLSHQPLAGTPEATYQMTVELLFEDLIEEGEDEL 471
Db 618 ANAQELTKDQEEEAFAFNQKHALQKAKEVSPMSAPRMPSTIEDRRRRHMSWEDRSSHL 677
QY 472 TERLSQH 478
Db 678 RERRRRH 684

RESULT 15
Q9NYZ5 PRELIMINARY; PRT; 2162 AA.
AC Q9NYZ5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CALCITUM CHANNEL ALPHAIE SUBUNIT, DELTA19 DELTA40 DELTA46 SPLICED
DE VARIANT (FRAGMENT).
GN CACNAIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miltman S., Agnew W.S., Malek J.A.;
RT "Exon Organization and Alternative Splicing of CACNAIE.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF223391; AAF37688.1;
DR EMBL; AF239258; AAF37688.1; JOINED.
DR EMBL; AF239259; AAF37688.1; JOINED.
DR InterPro; IPR000636; Cation_chan_non_1ig.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
FT NON_TER
SQ SEQUENCE 2162 AA; 244728 MW; 9D40173993B9E261 CRC64;

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Query Match 7.1%; Score 186.5; DB 4; Length 2162;
Best Local Similarity 20.5%; Pred. No. 5.1e-07;

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Matches 98; Conservative 84; Mismatches 184; Indels 113; Gaps 19;
QY 32 LMGGDPVPMSCRCRCSQODGOD-----RERTYFQNLPESTLSLVLTTANNPDVWIPA 87
Db 170 LGGFDPHPCGVGCGPAGYECKDWIGPNDGITQFNDNLFAVLTVFQCITMEGWTVL--- 226
QY 88 YSKNRAYA-----IFFIVTVIGSLFLMNLTAIYSQF-----RGYLMKSQTS 132
Db 227 YNTNDALGATWMLLYFPLIIIGSFVNLVLGVLGSEFAKEREVENRRAFMKLRQOO 286
QY 133 LFRRLGTRAAFEVLSMWEGGAFPOATRPGPSTSLRCPARSSSSATTTTLTWTGSSP 192
Db 287 IERELNGYRAMIDKAEVW-----LAENKNAGTSALEVLRATIKRSTTEMTDSSDE 341
QY 193 W-----QWCPFACS-----WCWMQMCCLSY--MTSS---WGFSTASLCT 229
Db 342 HCVDISSVGTPLARASIKSAKVDGVSFRRKRELRLISIRHMVKSQVFWYIVLSVALNT 401
QY 230 TCWSCCSRSLP-WACE-----GTCPTPATCLTGSSPLSCMR-P 265
Db 402 ACVAIVHNNQPOWLTHLLYYAEFLGLFLLEMSLKNYGMGPR---LYFHSSEFCDFG 457
QY 266 EMVGLL--SLMDMTRM-----LNLIVFRRLIIPSMKPMAYVASTVLGVOMRAFGGI 318
Db 458 VIVGSIIEVVAIFRPGTSEGISVLRALRLRIFKITKWAISLRNLVYSLSMSKSIISL 517
QY 319 LVVVY---YVFAIGINLFRGVIVALPGNSSLAPANGSAPCGSPOLEYMANNEDFPAA 375
Db 518 LFLFLFIVFVALLGMQLFGGRFNFNDGTPSA-----NFDTPPAA 557
QY 376 LVTLMLNVVNNM-OVFLDAYRRY---SGPWSKIYFVLMVLYSSVIVWNLFLALILENF 429
Db 558 IMTFVQILTGEDMNEVMYNGIRSGGVSGMWSAIFYIVLILFGNTTLNVFLAIAVDN 616

Search completed: October 8, 2002, 10:04:57
Job time : 72 secs

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